

18.4%; Score 174; DB 3; Length 1677;

Best Local Similarity 52.4%; Pred. No. 1.9e-40;
Matches 433; Conservative 0; Mismatches 360; Indels 33; Gaps 1;

```

Qy 60 CGTATCCCCAGCAGGAGTCCAGCTTGTGAAAGCTCGGCGCTTCCATCCGCGCT 119
Db 337 CATAGTTCGGAGAGAGAGGCTTGTGTGAGAGATTCGGAGATTCACAGACCT 396
Qy 120 GACGCGCGTTGATATTTTGAATTCCTTATGACGCGCGCTACCGCATTCGCT 179
Db 397 CGGCTCCGGGTTTCCACTCTGATCCCGCGCTGACCTTATTCCTACGTCACCT 456
Qy 180 GAAAGAAATCCCTTGAAGTACGTAACCGACAGGTCTGATCAGCGCGATTAATGCAATT 239
Db 457 CAAGAGAGAGACCATCCCTATCCCTACCAAGAGCCATCAACAAGACAGTACCAT 516
Qy 240 GACTGTGAAGCGCATCTATCTATTCAGATTAACGATCCCAATCCGCTCATACGCTTC 299
Db 517 ACAGATTGACAGCGCATCTATCTATGATGATGATGATGATGATGATGATGATGAT 576
Qy 300 GAGCACTACATTAATGCAATTAACCGACTTGGCCCAAGACGCTGCGCTTATGCG 359
Db 577 GAGAGATCAATCTATGCTGTCTTACATCTGACAAACCAACATGAGAGTGAATCG 636
Qy 360 GCGATGAGAGTTCAGCAAAAGCTTGAAGAAAGCGACGAAATCAACAGTACCGTCTC 419
Db 637 GAGATTAACCTTAAGTAAAGCTTGAAGAGAGATGATTAATGAGAAATTTGTAG 696
Qy 420 CGCCTCGATGAAGCGCGCGGCTTGGGCTGTGAATCTCCGTTACGAATCAAGAA 479
Db 697 TGCCATCAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 756
Qy 480 TTTGGTTCGCGCGAGAAATCTCTTGGCAATGAGAGAGAGAGAGAGAGAGAGAGAG 539
Db 757 CATATATCTCTAGAGAGAGATTAAGCAGGCTATGAGATGAGAGAGAGAGAGAGAG 816
Qy 540 AAAACGCGCCGCTATTCGCAATTCGAAAGCGCGTAAATTCGAACAAATCAACTTGCAG 599
Db 817 AAAACGCGCTCAATCTTGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 854
Qy 600 TGCTAGGCTGAAGCGCAATTCGAACATTCGAAGAGAGAGAGAGAGAGAGAGAGAG 659
Db 855 -----AGGCGCCAAATCTTGAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 903
Qy 660 GTCCAAATCGAGAGAAATTCGCGCGATCAACGCGCGCAAGAGAGAGAGAGAGAGAG 719
Db 904 ATCTGAAGAGAGCTATGTTGATCTAGCAACCGTGCAGAGGTGCGCTGAAGCAATCT 963
Qy 720 CTTGTTGCGAGAGCAATTCGCAAGCCATCCGTAATTCGCGCGCTTCAACCCA 779
Db 964 TGCCAAATCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1023
Qy 780 AGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 839
Db 1024 AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1083
Qy 840 TCTTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 885
Db 1084 TCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1129

```

RESULT 2
CNS090CF 931 bp mRNA linear HTC 08-JAN-2003
LOCUS
DEFINITION Single read from an extremity of a full-length cDNA clone made from
Anopheles gambiae total adult females. 5-PRIME end of clone
FK0A051B03 of strain 6-9 of Anopheles gambiae (African malaria
mosquito).

ACCESSION BX067627
VERSION BX067627.1 GI:27640908
KEYWORDS HTC
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Anopheles.
REFERENCE 1 (bases 1 to 931)

AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (06-JAN-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

FEATURES
source location/Qualifiers
1..931
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="6-9"
/db_xref="taxon:7165"
/clone="FK0A051B03"
/plasmid="pME18S-FL"
/note="end : 5-PRIME"

ORIGIN

Query Match 17.9%; Score 170; DB 3; Length 931;
Best Local Similarity 54.3%; Pred. No. 2.6e-39;
Matches 364; Conservative 0; Mismatches 305; Indels 1; Gaps 1;

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Qy 65 TCCCCAGCAGAGAGTCCAGCTTTCGAAAGAGCTCGGCGCTTCCATCGCGCTGACG 124
Db 256 TGCCCAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 315
Qy 125 CCGGTTGAATATTTTGAATTCCTTATTCAGACCGCGCTGCTTACCGCATTCGTTGAAG 184
Db 316 CCGGCTGAAGAGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 375
Qy 185 AATCCCTTGAAGAGTACGTAACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 244
Db 376 AATTCGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 435
Qy 245 TTGACGAGATCATCTATTTCCAAATGTAACGATCCCAACTGCTCATACGTTGAGCA 304
Db 436 TCGACGAGTGTCTGTACTCTGCGCATTCGACCGGCTACTGCGTGAAGTGAAGG 495
Qy 305 ACTCATTTATGCAATTAACCAAGTTCGCAACAGAGAGAGAGAGAGAGAGAGAGAG 364
Db 496 ACCGAGAGTTCATCAACCAAGTTCGCAACAGAGAGAGAGAGAGAGAGAGAGAGAG 555
Qy 365 TGAGTTGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 424
Db 556 TGTCACTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 615
Qy 425 TCGATGAAGCGCGCGGCTTGGGCTGTGAAGTCTCCGTTACGAATCAAGAGATTGG 484
Db 616 TCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 675
Qy 485 TTCGCGCGCAAGAAATCTCTGCGCAATGCAAGAGAGAGAGAGAGAGAGAGAGAG 544
Db 676 AGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 734
Qy 545 GCGCGCGATTTGCGCAATTCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 604
Db 735 GGGCGCGATCTCTGAGTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 794
Qy 605 AGCGTGAAGCGGAATTCGAATTCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 664
Db 795 AGCAGAGTCCGCGATCTCTGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 854
Qy 665 ATGCGGAGAAATGCGCGCATCAACCGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 724
Db 855 ATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 914
Qy 725 TTGCGGAAGC 734
Db 915 TGCGCAATC 924

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RESULT 3

CD789571
LOCUS CD789571 890 bp mRNA linear EST 01-JUL-2004
DEFINITION EST660932 RAB Rhipicephalus appendiculatus CDNA clone RABAJ94 5'
ACCESSION CD789571
VERSION CD789571.1 GI:49545245
SOURCE EST
ORGANISM Rhipicephalus appendiculatus
Rhipicephalus appendiculatus
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
Parasitiformes; Ixodida; Ixodidae; Ixodidae; Rhipicephalus.
1 (bases 1 to 890)
Nene, V., Lee, Y., Skilton, R., Mwaura, S., Quackenbush, J., Gardner, M.
and Bishop, R.
TITLE An index of genes transcribed in the salivary glands of
Rhipicephalus appendiculatus
JOURNAL Unpublished (2003)
COMMENT Other ESTs: EST660931
Contact: Vishwanath Nene
Parasite Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-610-5968
Fax: 301-838-0208
Email: nene@igr.org
Seq primer: M13 reverse.
Location/Qualifiers
1..890
/organism="Rhipicephalus appendiculatus"
/mol_type="mRNA"
/strain="Muguga"
/db_xref="taxon:34631"
/clone="RABAJ94"
/dev_stage="Adult"
/lab_host="E. coli strain DH10B-Tona"
/clone_lib="RAB"
/note="Organ: Salivary glands; Vector: pCMVSPORT6.0.ccd; Salivary glands were dissected on day four after initiation of feeding. Total RNA was prepared using acid guanidium thiocyanate-phenol-chloroform extraction. The CDNA library was custom prepared by Invitrogen Corporation. Briefly, first strand cDNA was primed using oligo(dT) containing a NotI site. Size fractionated double stranded cDNA was ligated to EcoRV-NotI cleaved vector and electroporated into E.coli. Library RAB was made from ticks infected with Theileria parva."

ORIGIN
Query Match 17.6%; Score 166.8; DB 6; Length 890;
Best Local Similarity 53.0%; Pred. No. 2.3e-38;
Matches 357; Conservative 0; Mismatches 317; Indels 0; Gaps 0;

QY 56 TTGTGCTATCCCCGAGAGAGTCCAGTGTGGAAGGCTCGGCGTTCCATCGCG 115
DB 192 TTATGTTGTACTCAACAGAGAGTGGGTGTGCGAGAGAGTGGAAAGTTTCGCGA 251
QY 116 CCTGACGCGCGGTGATATTTGATTTCCCTTTATCGACGCGTGCCTACCGCCATT 175
DB 252 TACTGAGGCCGCTTGAACCTGCTCTCCGTGATAGACGTGATAGCTGACAT 311
QY 176 CGCTGAAGAAATCCCTTTAGACGTACCCAGCCAGGCTTGACATCAGCGCGATATACG 235
DB 312 CACTCAAAAGAAATAGCATCGACATCCGACAGAGTCTGCATTAAGCTAGACAAAGTGA 371
QY 236 AATTGACTGTGACGCGCATCATCTATTTCCAGTAACGATCCCAACTGCGCTCATAG 295
DB 372 CGCTCAACATCGACGCGCTTCTTACCTGAAGTGTGACCCATATCGGCGACGCTAG 431
QY 296 GTTCGAGCACTATATGCAATTATACCGAGCTTCCCAAGAGAGCGTGCCTTCCGTTA 355
DB 432 GCGTCAGAGACCCCGAATTCGATTAAGAGCTGCGACAGACCAAGATGCGCTCGAG 491
QY 356 TCGGCGTATGAGTTGACAAACGTTGAGAGACGCGACGAATCAACATGATCCGTG 415

DB 492 TCGGCAAGATAGCGCTGACAGCGCTCTTCAAGAGCGCGAGATCTCTCAACATTCGCAATG 551
QY 416 TCTCCGCCCTTGATGAGAGCCCGCGGCTTGGGGTGAAGAGTCTCGCTACGAAATCA 475
DB 552 TGAATGCCATCAACAGAGCGAGCGGTGTGAGGATCTGTGCTGCGTACGAGATCC 611
QY 476 AGAATTGGTTCGCGCGCAAGAAATCCCTCCGCAATCAGAGCACAAAATTAACCGCGAAC 535
DB 612 GCGACATACGCTTCTTCAACAGCGGCTTCAACAGAGCATGCAATGCAATCGAAGCCGAG 671
QY 536 GCGAAAAAGCGCGCCGTATTCGCCGAATCGAAGCGCGTAAATCGAACAAATCAACCTTG 595
DB 672 GGAAGAAAGAGCGCGCACTTCTGAGTCTGAAGAAATGAAGAGACAGATATCAACGTAG 731
QY 596 CCAAGTGTGACGTGAGAGCCGAATTCGAACATCCGAAGGAGAGGCTACGCTGCGGTCA 655
DB 732 CCGAGGGCAAGCGCGCTGCGGCAATCTTGAGCTTGGAAGCGCAAAAGATGAGCTAATTA 791
QY 656 ATGCGTCAATGCGAGAAATTCGCGGCATCAACCGCGCAAGGCGAAGCGGAATCCC 715
DB 792 ACAAGCGCGATGCGAGGCGCAACGCGACCTTGCCAAAGCTGAGGCCAAGGCCAAGGCC 851
QY 716 TCGCGCTTGTGCC 729
DB 852 TTAGCAAGATAGCC 865

RESULT 4
AL541792 1048 bp mRNA linear EST 24-MAR-2004
LOCUS AL541792 Homo sapiens PLACENTA Homo sapiens CDNA clone CS0DE007YE18
DEFINITION 5-PRIME, mRNA sequence.
ACCESSION AL541792
VERSION AL541792.3 GI:45717369
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 1048)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:30546303.
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES
source
1..1048
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE007YE18"
/issue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN
Query Match 16.5%; Score 156.8; DB 1; Length 1048;

Best Local Similarity 50.6%; Pred. No. 2.4e-35;
Matches 432; Conservative 1; Mismatches 388; Indels 33; Gaps 1;

```
Qy 62 TCAATCCCCAGAGAGAGTCCAGCTGTGCGAAAGCGTGGGGCTTTCCATGCGCCCGCA 121
Db 2 TCGTCCGCGACAGAGAGCGCTGGGGTGGAGCGAATGGCGGATTTCCACCGGATCTGG 61
Qy 122 CGGCGCGTTTGAATATTTGATTCCTTTATCGACCGCGTGGCTTACCCGCTATTCGCTGA 181
Db 62 AGCCGTGGTTGAATCCTCATCCCTGTGTTAGACCGGATCCGATATGTGACAGTCTCA 121
Qy 182 AAGAAATCCCTTTAGACGTACCCAGCCAGCTGTGCATACCGCGGATATATGCAATTGA 241
Db 122 AGGAAATGTGATCAACGTGCGCTGAGCAGTGGCTGTGACTCTCGACAAATGTAATCTGCG 181
Qy 242 CTGTTGAGCGATCATATATTTCCAGTAACGATCCCAACTGCGCTCATACGCTTCA 301
Db 182 AAATCGAGAGAGCTTTTACCTGCGCATATGAGACCTTTCAAGGCAAGCTACGCTGG 241
Qy 302 GCAACTACATTATGGCAATTAACCGACTTGGCCCAAGACGCTGGCTTCCGTTATCGGCG 361
Db 242 AGGACCCGTGATATCCCTCACCGCTAGCTCAAAACAACATGATCAAGAGCTCGCA 301
Qy 362 GTATGAGATTGACAAAAGCTTTGAAAGACGCGAAGAAATCAACAGTACCGTCTTCGG 421
Db 302 AACTCTCTGTGACAAAGTCTTCGCGAAGCGGAGTCCCTGAATGCGACATTTGTGATG 361
Qy 422 CCCTCGATGAAGCGCGCGGCTTGGGGTGTGAAAGTCTCCGTTACCAAAATCAAGATT 481
Db 362 CCATTCACCAAGCTGTGATGCTGGGGTATTCGCTGCTCCGTTATAGATCAAGGATTA 421
Qy 482 TGGTTCGCGCGAAGAAATCTTGGCGGATGCGAGGACCAAAATTAACCGCGAAGCGGAA 541
Db 422 TCCATGTGCCACCCCGGGTGAAGAGTATATGACATGACAGTGAAGGACAGCGCGGA 481
Qy 542 AACGCGCCGATATGCGCAATCCGAAGCCGTAATGAAACAATCAACTTGGCAGTG 601
Db 482 AACGGGCGACAGTTCTAGAGTCTGA-----GG 508
Qy 602 GTACGCGTGAAGCGCAAAATCCAAATCCGAAGCGAGGCTCAAGCTCGGCTCAATGCT 661
Db 509 GGAACCGAGAGTCCGCGCATATGTGCGAAGAGGAAACAGGCCCAAGATCTCGGCT 568
Qy 662 CCAATGCGGAGAAATATCGCCGATCAACCGCGCAAGCGAAGCGGATCCCTGCGGCC 721
Db 569 CCGAGCGAAGAAAGCTGAACATATCAAGCGACGAGAGAGGCCAGTCAAGTTCTGG 628
Qy 722 TTGTTGCGGAAGCAATGCGCAAGCCATCGTCAATTTGCGCGCCCTTCAAAACCAAG 781
Db 629 CGAAGCGCAAGGCTTAAGCTGAAGCTATTCGAATCTGGCTGCAAGCTCTGACACAACTA 688
Qy 782 GCGGGGCGGATGCGGTCAATCTGAAGATTGGGAAACAATACGTAGCCGCTTCAACAATC 841
Db 689 ATGAGAGATGACAGCTTCACTGACTGTGGCGGACAGATATGTCAAGCCGTTCTCAAAAC 748
Qy 842 TTGCGAAGAAAGCAATATGCTGATATGCGCGCAATGTTGCGGACATCGGAGCGCTGA 901
Db 749 TGGCGCAAGACTCCAAACTATCTACTGCTCCCAACCTTGGGATGTCAACGACATGG 808
Qy 902 TTTCTGCGCGCATG 915
Db 809 TGGCTCAGGCGCATG 822
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RESULT 5
BI486916
LOCUS
DEFINITION
BI486916 673 bp mRNA linear EST 28-AUG-2001
R070403.5 prime RE Drosophila melanogaster normalized Embryo pfic-1
Drosophila melanogaster cDNA clone R070403.5 similar to CG2970:
R070403.5 (0) located on: 2R 60A12-60A13; 05/17/2001, mRNA
sequence.

ACCESSION
BI486916
VERSION
BI486916.1 GI:15326585

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

EST.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 673)
Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B.,
Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E.,
George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G.,
Miera, S., Mangall, C. J., Nunoo, J., Pacleb, J., Paragas, V., Park, S.,
Phouanavong, S., Wan, K., Yu, C., Lewis, S. E., Celniker, S. and
Rubin, G. M.
BDGP/HMTI RE Drosophila EST Project
Unpublished (2001)
Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: <http://www.fruitfly.org/EST/est@fruitfly.berkeley.edu>
hit genomic: AB003462: arm:2R [18701964,19002505]
estimated-cyto: 60A1-60B4: 05/17/2001
Plate: RE.704 row: A column: 3
High quality sequence stop: 623.
Location/Qualifiers

FEATURES
source
1..673
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/clone="RE70403"
/sex="male and female"
/dev_stage="0-24 hours mixed stage embryonic"
/lab_host="DHS-alpha Tona"
/clone_id="RE Drosophila melanogaster normalized Embryo
pfic-1"
/note="Organ: embryo; Vector: pfic1; Site: 1; XhoI; Site: 2;
BamHI; Library was kindly generated by Piero Carninci at
the RIKEN. The library was normalized and excised using
Cre recombinase. Plasmid cDNA library."

ORIGIN

Query Match 16.5%; Score 156.6; DB 4; Length 673;
Best Local Similarity 52.6%; Pred. No. 2.4e-35;
Matches 339; Conservative 0; Mismatches 305; Indels 0; Gaps 0;

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Qy 29 CCGTCCGCTTTTGGCTTCAATCTTTGTGCTATCCCGACAGAAAGTCCACGTTG 88
Db 26 CGGTCCGCGGACGCTCACTCAATCCGATCGTCTCTCGTTTCCAGGCTGGGGTGG 85
Qy 89 TCGAAAGGCTCGGGCGTTTCATGCGGCCCGTGAAGCGCGGTTGATATTTGATTCCT 148
Db 86 TGGAGCGCATGCGGCGCTTTCACAGATTTTGAACCCCGGACTCAACATTAAGTCCCG 145
Qy 149 TTATCGACCGCGGTGCTTACCGCATTCGCTGAAGAAAGAAATCCCTTGAAGTACCGACC 208
Db 146 TGGGCGAAGAAATATATATGCTCCAGAGCTGAAGAAATTTGCATGATGTGCCAAAC 205
Qy 89 TCGAAAGGCTCGGGCGTTTCATGCGGCCCGTGAAGCGCGGTTGATATTTGATTCCT 148
Db 86 TGGAGCGCATGCGGCGCTTTCACAGATTTTGAACCCCGGACTCAACATTAAGTCCCG 145
Qy 149 TTATCGACCGCGGTGCTTACCGCATTCGCTGAAGAAAGAAATCCCTTGAAGTACCGACC 208
Db 146 TGGGCGAAGAAATATATATGCTCCAGAGCTGAAGAAATTTGCATGATGTGCCAAAC 205
Qy 209 AGGTCTGCATACCGCGGATATATGCAATTTGATGAGCGGATCATATTTTCAAG 268
Db 206 AGAGCGCTATTAACCTCGACAAAGCTGAGACCTGAGCATGACGCGGCTCTCACTTGGCA 265
Qy 269 TAAACGATCCCAACTGCGCTCATACGCTTTCGAGCAACTATATATGCAATTAACGAGC 328
Db 266 TCATTGATCCGTAACAAAGCTCGTACGCGGTGAGAGATTCGGAATGCGCAATAACAAAC 325
Qy 329 TTGCGCAAGACGCGCTGCTTCCGTTATCGGCGGATGAGATTGACAAACGTTGAAG 388
Db 326 TGGCGCGAAGACGATGATGAGTGGAGCTGGGCAAGATGTCCATGACAAAGTCTTCCACG 385
Qy 389 AACGCGAAGAAATCAACAGTACCGTCTCTCGGCTCGATGAGCGCGCGGGGCTTGGG 448
Db 386 AAAGGAGTCCCTCAAGGTGAGATGCTGATCAACAAAGCGCAGCGAGCGGCTGGG 445
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QY 449 GTGTGAAGTCTCTGTTAGCAATTCAGATTGGTTCCGCCGCAAGAAATCTTCCG 508
 Db 446 GCATCGCTGTCTGGATACGAGATCCGTGATATTCAGCTGCCACGAGGTTCCAGAG 505
 QY 509 CAATGACGACCAATTTACCCGCCGAAACGCGCCGTTATTCGCAATCCGAG 568
 Db 506 CGATGCAATGCAATGAGAGCGCGGCGGAAAGCGGCTATTTCTCGAATCGAGG 565
 QY 569 GCCGTAATTCGAACCAATCAACTTGGCAGTGTACGCTGAGAGCCGAAATTCACAAAT 628
 Db 566 GTGTTCCGAGGCGCAAAATCAACATAGCCGAGGCGAAGCAAGCTAGATTGAGCT 625
 QY 629 CGAAGGCGAGGCTCAGGCTCGCTCAATGCTCAATGCGAG 672
 Db 626 NCGAGGCGGAGCGGCGAGGACATCAATTAAGCGCAGCGAGAG 669

RESULT 6 413 bp DNA linear GSS 17-JAN-2003
 BZ626199
 LOCUS ih44c01.b1 MGS-Sbicolorf (DH5a methyl filtered) Sorghum bicolor
 DEFINITION genomic clone ih44c01 5', genomic survey sequence.
 ACCESSION BZ626199
 VERSION BZ626199.1 GI:27778284
 KEYWORDS GSS.
 SOURCE Sorghum bicolor (sorghum)
 ORGANISM Sorghum bicolor
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Sorghum.
 1 (bases 1 to 413)
 Rabinowicz, P.D., O'Shaughnessy, A.L., Balija, V., Dedhia, N.,
 Katzenburger, F., King, L., Miller, B., Muller, S., Nascimento, L.,
 Zuteven, T., Palmer, L., McCombie, W.R. and Martienssen, R.A.
 Genomic shotgun sequences from Sorghum bicolor (methyl-filtered)
 Unpublished (2002)
 CONTACT: W. Richard McCombie
 Lila Annenberg Hazen Genome Sequencing Center
 Cold Spring Harbor Laboratory
 PO Box 100, Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8884
 Fax: 516 367 8874
 Email: mcombie@cshl.org
 Plate: ih44 row: c column: 01
 Seg primer: -21M13univFwd
 Class: Shotgun
 High quality sequence stop: 413.
 Location/Qualifiers
 1..413
 /organism="Sorghum bicolor"
 /mol_type="genomic DNA"
 /db_xref="taxon:4558"
 /clone="ih44c01"
 /lab_host="DH5a"
 /note="lib="MGS-Sbicolorf (DH5a methyl filtered)"
 /note="Site 1: Xba I; Site 2: Xba I; The vector was
 digested with Xba I and one nucleotide was added by fill in
 in the recessive 3' end. The genomic DNA was nebulized,
 end repaired, adaptor ligated and size fractionated using
 sephadex. The resulting fragments were between 0.8 and 3
 kb and were cloned into the vector (.x/y reads in M13mp19,
 b/g reads in pUC19). The same ligation was transformed
 into DH5a."

ORIGIN
 Query Match 16.5%; Score 156; DB 8; Length 413;
 Best local Similarity 63.9%; Pred. No. 3.2e-35;
 Matches 271; Conservative 0; Mismatches 120; Indels 33; Gaps 1;
 QY 473 TCAGAGATTGGTTCCGCCGCAAGAAATCTTCCGCAATGCGGCAATTAACGCCG 532
 Db 11 TCAGAGACTGACCCGCCCAAGAAATCTTGCACGCGCATGACGCCACAGATCACGCCG 70

QY 533 AAGCGAAAAAGCGCCCGTATTCGCAATCCGAAGCCGTAATTCGAACCAATCAACC 592
 Db 71 AGCGGAAAAAGCGCCCGTATTCGCAATCCGAAGCCGTAATTCGAACCAATCAACA 130
 QY 593 TTGCGATGTTGTCAGCGTGAAGCCGCAAAATTCGAATTCGAAGCGAGGCTCAGGTCGG 652
 Db 131 TCAGCAAGCGGTGAAGCGGCAAGCCGCAATTCGCGCTCGAAGGCGAAGAGCGCTTC -- 188
 QY 653 TCATATGCTCCATATGCGGAGAAATTCGCGCCGATCAACCGCGCAAGGCGGAGCGAAT 712
 Db 189 -----CATCAACCGTGCAGAGGCGCAAGGCTTCGG 217
 QY 713 CCTGCGGCTTTGTTCCGAGCAATGCGGAGCAATCCGTTCAATTCGCGCGCTTC 772
 Db 218 CCATCTCGCATGCGCAAGCGCGGCAAGCGGCAAGCGGCAAGCGCGCTTCGATCG 277
 QY 773 AAACCCAGGCGGCGGCGGATGCGGTCAATCTGAAGATTGCGGAAATATGATGCGGCT 832
 Db 278 AGCAGCGGCGGCGGTTTCGATGCGGTCAACTGAAGGTGCGGAGCATATGATGCGCT 337
 QY 833 TCACCAATCTTCCCAAGAAAGCAATACGCTGATTAATCCCGCCCAATGTTGCCGACATCG 892
 Db 338 TCAGCAAGCTGGCGCAAGCAATTAATCAATCAATGTCGCGCCCAATCTGGCGACATGA 397
 QY 893 GCAG 896
 Db 398 GCGG 401

RESULT 7 768 bp mRNA linear EST 23-SEP-2003
 CA065919
 LOCUS SCBPAD1049A04.g AD1 Saccharum officinarum cDNA clone SCBPAD1049A04
 DEFINITION 5', mRNA sequence.
 ACCESSION CA065919
 VERSION CA065919.1 GI:34917443
 KEYWORDS EST.
 SOURCE Saccharum officinarum
 ORGANISM Saccharum officinarum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
 complex.
 1 (bases 1 to 768)
 Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
 The libraries that made STUCST
 Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
 CONTACT: Arruda P
 Centro de Biologia Molecular e Engenharia Genetica
 Universidade Estadual de Campinas
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil
 Tel: 55 19 3788 1137
 Fax: 55 19 3788 1089
 Email: parruda@unicamp.br
 clone distribution: clone distribution information can be found
 through the Brazilian Clone Collection Center (BCCC) at
 http://www.bcccenter.fcav.unesp.br
 Plate: 049 row: A column: 04
 Seg primer: T7 Promoter Primer.
 Location/Qualifiers
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RESULT 9
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 VERSION AY408615.1 GI:39764586
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 1071)
 AUTHORS Clark,A.G., Glandowski,S., Nielson,R., Thomas,P., Kejarimal,A.,
 Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J.,
 Adams,M.D. and Cargill,M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 TITLE Science 302 (5652), 1960-1963 (2003)
 JOURNAL
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 1071)
 AUTHORS Clark,A.G., Glandowski,S., Nielson,R., Thomas,P., Kejarimal,A.,
 Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J.,
 Adams,M.D. and Cargill,M.
 Direct Submision
 TITLE Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 JOURNAL
 COMMENT This sequence was made by sequencing genomic exons and ordering
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 Best Local Similarity 50.6%; Pred. No. 5.5e-35;
 Matches 432; Conservative 0; Mismatches 389; Indels 33; Gaps 1;
 Oy 62 TCATCCCCAGAGGAGGCAAGTCAAGTGTGAAAGGCTCGAGCGCTTCATCGCGCCCTGA 121
 Db 119 TGTGCGCGAGAGGAGGCGCTGGTGTGAGAGCAATGGGCGGATTCACCGGATCTGG 178
 Oy 122 CGGCGGTTTGAATTTTGAATTCCTTATTCGACCGCGTGGCTTACCGCATTCGCTGA 181
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 Oy 182 AAGAAATCCCTTGAAGAGTACCGACGAGCTGTGCATCAGCGCGCATTAATGCAATTGA 241
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 Oy 242 CTGTGAGCGGCAATCTATTTTCAGAGTAACGATCCCAAGCTCGGCTCATACGTTTCA 301
 Db 299 AATATCATGAGTCTTACTGCGCATATGAGACCTTTACAGGCAAGCTACGAGTGTGG 358
 Oy 302 GCAACTACATTAATGCAATTAACCAAGCTTGCCTGAGAGAGAGCTGCTTATTCGAGG 361
 Db 359 AGGACCTGAGTATGCGTCAACCCAGCTAGCTCAAAACATGATGAGATCAGAGCTGGCA 418
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 (human).
 ACCESSION CR594962
 VERSION CR594962.1 GI:50475769
 KEYWORDS HTC; CNSTL cDNA.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 1073)
 AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 REMARK Contact : Feng Liang Email : fliang@life.techn.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue
 Carlsbad, CA 92008
 REFERENCE 2 (bases 1 to 1073)
 TITLE Genoscope.
 AUTHORS Direct Submision
 TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
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 ORIGIN

Query Match 16.4%; Score 155.6; DB 3; Length 1073;
Best Local Similarity 50.6%; Pred. No. 5.5e-35;
Matches 432; Conservative 0; Mismatches 389; Indels 33; Gaps 1;

QY 62 TCATCCCCCAGCAGAAATCCAGCTTGTCCGAAAGGCTGGGGCTTTCCATGGCCCTCGA 121
DB 2 TCGGCCCGCAGCAGAGGCTGGGGGTGGAGCGAATGGGCGAATTCACCGGATCTCGG 61
QY 122 CGGCGCGGTTGAATTTTGAATCCCTTATCCGAGCGGCTCCACCGCATTCGCTGA 181
DB 62 AGCTGGGTTGAACATCTCTCATCTCTGTGTGATGACCGGATCGATATGTGAGAGCTTCA 121
QY 182 AAGAAATCCCTTTAGACGTACCCAGCGAGGTCTGCATCACCGCGCATTAATACGAATTGA 241
DB 122 AGAAATATGTATCAACGTGCTGAGAGGTGGGTGTGACTGTGACCTGCAATGAACTCTGC 181
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DEFINITION 5' mRNA sequence.
ACCESSION BUS08142
VERSION BUS08142.1 GI:22814375
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1095)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM14057 Row: m Column: 22
High quality sequence stop: 760.
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Average insert size 2.1 kb."

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Query Match 16.4%; Score 155.6; DB 5; Length 1095;
Best Local Similarity 50.6%; Pred. No. 5.6e-35;
Matches 432; Conservative 0; Mismatches 389; Indels 33; Gaps 1;

QY 62 TCATCCCCCAGCAGAAATCCAGCTTGTCCGAAAGGCTGGGGCTTTCCATGGCCCTCGA 121
DB 12 TCGGCCCGCAGCAGAGGCTGGGGGTGGAGCGAATGGGCGAATTCACCGGATCTCGG 71
QY 122 CGGCGCGGTTGAATTTTGAATCCCTTATCCGAGCGGCTCCACCGCATTCGCTGA 181
DB 72 AGCTGGTGTGAACATCTCATCTCTGTGTAGACCGGATCCGATATGTGACAGATCTCA 131
QY 182 AAGAAATCCCTTTAGAGTACCCAGCGATGCTGCATACGCGGATTAATACGAATTGA 241
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QY 542 AACGCGCCGATATGCGGAATCCGAAGCGGTAAATGAAACAAATCAACCTTCCAGTG 601
DB 492 AACGGGCCACAGTTCTAGAGTCTGA-----GG 518

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LOCUS		full-length cDNA clone CS0DJ011YA06 of T cells (Jurkat cell line)	
DEFINITION		Cot 10-normalized of Homo sapiens (human).	
ACCESSION		CR612088	
VERSION		CR612088.1 GI:50492895	
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ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
TITLE		1. (bases 1 to 1103)	
JOURNAL		Li, W.B., Gruber, C., Jessee, J., and Polayes, D.	
REMARK		Full-length cDNA libraries and normalization	
		Unpublished	
		Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue	
		2. (bases 1 to 1103)	
		Genoscope.	
REFERENCE		Direct Submission	
AUTHORS		Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :	
TITLE		BP 191 91006 EVRY cedex - FRANCE (E-mail : segre@genoscope.cns.fr	
JOURNAL		- Web : www.genoscope.cns.fr)	
		1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime	
COMMENT		into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library	
		was normalized. Library was constructed by Life Technologies, a	
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182	AAGAAATCCCTTTTGAAGTACCCGACCGAGGTCTGTCATCAGCGCGATTAATACGAAATGA			241
163	AGGAAATTTGTCATCAAGTGTGCTGAGGAGTGGGTGTGATCTTCGACAAATGTAATCTGTC			222
242	CTGTTGACGGCATCATCTATTTCCAGTAACCGATCCCAACTTCGCTCATTCGTTTGA			301
223	AAATCGATGAGTCTTTTACCTGCGCATCATGACCTTTCAAGGCAAGCTACGGTGTGG			282
302	GCAATCATATTATGGCAATTAACCGAGTTGCCCAAGACGAGTGGCTTCCGTTACGGGC			361
283	AGGACCTCGATGATCCGCTCACCCAGTAGTCTCAACACATGATGATCAGAGCTGGCA			342
362	GTATGAGATTGGAACAAACGTTTGAAGACGCGACGAAATCAACAGTACCGTCTCCG			421
343	AACTCTCTCTGGAACAAAGTCTTCGGGGAACGGGAGTCCCTGAATGCCAGCATTTGTGATG			402
422	CCCTCGATGAAGCCCGCGGGGCTTGGGTGTGAAGTCTTCCTTTAGGAATCAAGGATTT			481
403	CCATCAACCAAGCTGTGACTGTCTGGGGTATCCGCTCTCCGTTATGAGATCAAGATA			462
482	TGTTTCCGCGCAAGAAATCCTTGGCGCAATGACGAGCAAAATTAACGCGCAACGCGAAA			541
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542	AACGCGCCGCTATTGCGGAATCCGAAAGCGGTAATGAACAATCAACTTGCACATG			601
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652	CCAATGCGCGAAGAAATCGCCGCGCATCAACGCGCAAGCGAAGCGGAATCCTTGGCC			721
610	CCGAAAGCAAGAAAGGCTGACAGATTAATACGACGACGAGAGGCCAGTGCAGTTCG			669
722	TTGTTCCGGAAGCAATGCGGACGACATCGTCAAAATTTGCCGCGCCCTTCAACCCAG			781
670	GGAAGGCCAAGGCTTAAGGTGAACTATTGCAATCTCGGCTGCGACTCTGACACAACTA			729
782	GCGGGGCGGATGCGGTCAATCTGAAGATTTGGGAAACATACGTAGCGCGCTTCAACATC			841
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902	TTTCTGCCGCGCATG			915
850	TGGCTCAGGCCATG			863

JOURNAL Unpublished
 REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue
 2 (bases 1 to 1142)
 REFERENCE Genoscope.
 AUTHORS Direct Submission
 TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
 JOURNAL BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
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 Best Local Similarity 50.6%; Pred. No. 5.6e-35;
 Matches 432; Conservative 0; Mismatches 389; Indels 33; Gaps 1;

62 TCATCCCCCAGAGAGGACGTCGTCGAAAGGCTGGGGGTTTCATCGCCCGCTGA 121
 109 TCGTCCCGGAGAGAGGCTGGGGTGGAGCGCAATGGCCGATTCCACCGCATCTCG 168
 122 CGGCGGTTTGAATATTTGATTCCTTTATCGACCGCGTGGCTTACCGCATTCGTGA 181
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 902 TTTCTGCGGCGCATG 915
 916 TGGCTCAGGCCATG 929
 Db
 ORIGIN
 Query Match 16.4%; Score 155.6; DB 3; Length 1196;
 Best Local Similarity 50.6%; Pred. No. 5.7e-35;
 Matches 432; Conservative 0; Mismatches 389; Indels 33; Gaps 1;

62 TCATCCCCCAGAGAGGACGTCGTCGAAAGGCTGGGGGTTTCATCGCCCGCTGA 121
 133 TCGTCCCGGAGAGAGGCTGGGGTGGAGCGCAATGGCCGATTCCACCGATCTCG 192
 122 CGGCGGTTTGAATATTTGATTCCTTTATCGACCGCGTGGCTTACCGCATTCGCTGA 181
 193 AGCCTGGTTTGAACATCTCATCTCTGTATGACCGGATCCGATATGTGAGAGTCTCA 252
 182 AAGAAATCCCTTTAGAGCTACCGAGCGATGTGATCAGCGCGCATATACGAATGA 241

REFERENCE
 AUTHORS Direct Submission
 TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
 JOURNAL BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 FEATURES
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 Location/Qualifiers
 1..1196
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DJ012YK06"
 /tissue_type="T cells (Jurkat cell line) Cot
 10-normalized"
 /plasmid="pCMVSPORT_6"

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 Db 313 AAATGATGAGTCTTTAAGTCCGATCATGACCTTTACAAAGCAAGCTACGGTGTGG 372
 Qy 302 GCAATACATTAATGCAATTAACCGCTTGGCCCAAGCGCTGGGTTCCGTTACGGGCG 361
 Db 373 AGGACCTGAGTATCCGCTGACCTGAGTAAAGTCAAGCAAGTGAATGAGCTGGCA 432
 Qy 362 GTATGAGTGTGGAAGAAAGTTTGAAGAACGCAAGCAATCAAGTACCGTCTCG 421
 Db 433 AACTCTCTGTGACAAAGTCTTCGGGAAGGGAAGTCCCTGATGCGCAGCATTTGGATG 492
 Qy 422 CCTTGATGAAAGCCCGGGGCTTGGGAGTGAAGTCTCTGTTACGAATCAAGATT 481
 Db 493 CCATCAACCAAGCTCTGACTGCTGGGGTATCCGCTGCTCGTTATGAGATCAAGATA 552
 Qy 482 TGGTCCCGCCGGAAGAAATCCTTCGCGAATGCAAGCAATTAACCGCCGAAGGAAA 541
 Db 553 TCCATGTGCGACCCCGGGTGAAGAGTCTATGCAAGTGAAGTGAAGCGAGCGGCGGA 612
 Qy 542 AACGGCCCGTATTTGCGCGAATCCGAAGCGCGTAAATCGAACAATCAACTTGGCAGTG 601
 Db 613 AACGGCCCAAGTTCTAGAGTCTGA-----GG 639
 Qy 602 GTACAGCTGTAAGCCGAATTCACAATCCGAAGCGAGGCTCAGGCTGCGTCAATGCT 661
 Db 640 GGAACCGAAGTCCGCGCATTAATGTCGAGAAAGGAAAGGAAAGGCGCCAGATCTGGCT 699
 Qy 662 CCAATGCCGAGAAATTCGCCGATCAACCGCGCCAAAGCGAAGGGAATCCCTGCGC 721
 Db 700 CCGAAGCAAGAAAGGCTGAACAGATTAATCAGGCAAGGAGAGGCGAGTGAAGTCTGG 759
 Qy 722 TTGTTGCGAAGCAATGCGAAGCATCGCTCAATTTGCGCGCGCTTCAACCCAG 781
 Db 760 CGAAGGCCAAGGCTAAAGCTTAAGCTTAATTCGAATCTGCTGCAAGTCTGACACAACTA 819
 Qy 782 GCGGGCGGATCGGCTCAATCTGAAGATTGCGGAACATACGTAAGCGGCTTCAACATC 841
 Db 820 ATGAGATGCAACAGTCTTCACTGACGTGGCGGAGATATGTCAGCGGTTCTCCAAAC 879
 Qy 842 TTGCGAAGAAAGCAATACGCTGATTATGCCCGCCCAATTTGCGCGACATCGGCAAGCTTA 901
 Db 880 TGGCAAGGACTCAACACTATCTACTGCTCCCTCCAAACCTGGCGATGTCACAGCATG 939
 Qy 902 TTTTGGCGGCGATG 915
 Db 940 TGGCTCAGGCGATG 953

RESULT 15
 LOCUS CR610520 1199 bp mRNA linear HTC 21-JUL-2004
 DEFINITION Full-length cDNA clone CS0D008YL10 of T cells (Jurkat cell line)
 ACCESSION CR610520
 VERSION CR610520.1 GI:50491327
 KEYWORDS HTC; CDS; cDNA.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCES
 1 (bases 1 to 1199)
 Li, W. B., Gruber, C., Jessee, J. and Polyes, D.
 Full-length cDNA libraries and normalization
 Unpublished
 CONTACT : Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue
 2 (bases 1 to 1199)
 Genoscope.
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REMARK

JOURNAL
 Submitted (20-JUL-2004) Genoscope - Centre National de Sequençage :
 BP 191 91006 Evry cedex - FRANCE (E-mail : sequefgenoscope.cns.fr)
 - Web : www.genoscope.cns.fr
 COMMENT
 1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
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 location/Qualifiers
 1..1199
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D008YL10"
 /cissue_type="T cells (jurkat cell line) Cot
 10-normalized"
 /plasmid="pCMVSPORT_6"
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 Query Match 16.4% Score 155.6; DB 3; Length 1199;
 Best Local Similarity 50.6% Pred. No. 5.7e-35;
 Matches 432; Conservative 0; Mismatches 389; Indels 33; Gaps 1;
 Qy 62 TCATCCCCAGCAGAGATCCACGTTGTGAAAGGCTCGGCGTTTCATCGCGCCTGA 121
 Db 142 TGTGCGCCGAGAGAGAGGCGCTGGGTGTGAGCGCAATGGGCGATTTCACCGGATCTCG 201
 Qy 122 CGGCGGTTTGAATTTTGAATTTGATTCCTTTATGACCGCGGTGCTTACCGCCATTGCTGA 181
 Db 202 AGCTGGTTTGAACATCTCTCCTGTTGATGACCGGATCGGATATGTCAGAGTCTCA 261
 Qy 182 AAGAAATCCCTTAAAGTACCGACCGAGTCTGATACACCGCGATATATAGCAATTGA 241
 Db 262 AAGAAATGTCAATCAACGCTGAGCAGTGGCTGTGATCTTCAACATGTAATCTGCG 321
 Qy 242 CTGTTGACGGCATCTATTTTCAAGTAACCGATCCCAACTCCGCTCATACGGTTGCA 301
 Db 322 AATGATGAGATCTCTTATCTGCGCATCATGAGACCTTTACAAAGCAAGTACGGTGTGG 381
 Qy 302 GCACTACATTAATGCAATTAACCGATTTGCCAAGCAAGCGTGGCTTCCGTTATCGGCG 361
 Db 382 AGGACCTGAGTATCCGCTCACCGAGTACTCAACCAACATGATGAGTCAAGTCTGGCA 441
 Qy 362 GTATGAGTGTGACAAACGTTTGAAGACGCAAGAAATCAACAGTACCGTCTCGG 421
 Db 442 AACTCTCTGTGACAAAGTCTTCGGAACGGAAGTCCCTGATGCGCAGATTTGGATG 501
 Qy 422 CCTGATGAAAGCGCGCGGCTTGGGGTGTGAAGTCTCCGTTACGAATCAAGATT 481
 Db 502 CCATCAACCAAGCTCTGACTGCTGGGTATCCGCTGCTCCGTTATGAGATCAAGATA 561
 Qy 482 TGGTCCCGCGAAGAAATCCTTCGCGAATGCAAGCAAGCAATTAACCGCGAAGCGGAAA 541
 Db 562 TCCATGTGTCACCCCGGGTGAAGAGTCTATGCAATGAGTGAAGGAGCGGCGGA 621
 Qy 542 AACGGCCCGTATTTGCGCGAATCGGAAGCGCTTAATAATCAACAACTTGGCAGTG 601
 Db 622 AACGGCCCAAGTTCTAGAGTCTGA-----GG 648
 Qy 602 GTACAGCTGTAAGCCGAATTCACAATCGGAAGGCGAGGCTCAGGCTGCGTCAATGCGT 661
 Db 649 GGAACCGAAGTCCGCGCATTAATGTCGAGAAAGGGAAGAAAGGCGCCAGATCTGGCTT 708
 Qy 662 CCAATGCCGAGAAATTCGCCGATCAACCGCGCAAGGCGAAGCGAATCCCTGCGCC 721
 Db 709 CCGAAGCAAGAAAGGCTGAACAGATTAATCAGGCAAGGAGAGGCAAGTCAAGTCTGG 768
 Qy 722 TTGTTGCGAAGCAATGCGGAGCATTCGTAATTTGCGCGCGCTTCAACCCAG 781
 Db 769 CGAAGGCCAAGGCTAAAGCTGAAGCTATTCGATCTGCTGCTGACACAACTA 828
 Qy 782 GCGGGCGGATCGGCTCAATCGAAGATTGCGGAACATACGTAAGCGCGCTTCAACATC 841

Db 829 ATGAGATGCGAGCAGCTTCACTGACTGTGGCGGAGCATATGACGCGCTTCTCCAAAC 888
Qy 842 TTGCCAAGAAGAAATACGCTGATTTATGCGGCAATGTTGCGGACATGCGGAGCCCGA 901
Db 889 TGGCCAAAGACTCCAAACCTATCTACTGCTCCCTCCACCCCTGGGATGTCAACGACATGG 948
Qy 902 TTTCTGCGCGCATG 915
Db 949 TGGCTCAGGCCATG 962

RESULT 16
CR608510 1206 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0DK006YK04 of HeLa cells Cot 25-normalized
DEFINITION
ACCESSION CR608510.1 GI:50489317
VERSION CR608510.1
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1206)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
Genoscope.
2 (bases 1 to 1206)
REFERENCE Direct Submission
AUTHORS Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
TITLE BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr
JOURNAL 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source
location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="CS0DK006YK04"
/tissue_type="HeLa cells Cot 25-normalized"
/plasmid="pCMVSPORT_6"

Query Match 16.4%; Score 155.6; DB 3; Length 1206;
Best Local Similarity 50.6%; Fred. No. 5.7e-35;
Matches 432; Conservative 0; Mismatches 389; Indels 33; Gaps 1;

ORIGIN
Query 62 TCATCCCCCAGAGAGATCCAGCTGTGCGAAGGCTGGGAGGTTTCATGCGGCCCTGA 121
Db 142 TCGTCCCGCAGAGAGAGCTGGGAGGTTGAGCGCAATGGCGGATTCACCGGATCTCG 201
Qy 122 CGGCGGTTTGAAATTTGATTCCTTTATCGACCGGCTGCGCTACCGGCATTCGCTGA 181
Db 202 AGCGTGGTTTGAATCTCTCATCCCTGTGTTAGACCGGATCGATATGTGACAGAGTCA 261
Qy 182 AAGAAATCCCTTTAGAGTACCGACGAGCTGTGATACGCGGATTAATACGAATGA 241
Db 262 AGGAAATGTATCAACGTGCTGAGAGTGGCTGTACTCTCGACAAATTAATCTCTGC 321
Qy 242 CTGTTGAGGAGATCATCTATTTCCAGTAACGATCCAACTCGCCCTCATACGGTTGA 301
Db 322 AAATGAGAGAGTCTTTTACCTGCGCATATGAGACCTTTACAGGCAAGACTACGGTGG 381
Qy 302 GCAACTATACATTATGCAATTAACCGAGCTTGGCCAAACGACGCTGCTTCCGTTATCGGGC 361

Db 382 AGACCCCTGAGTATGCCGTGACCCAGCTAGCTCAACCAACCATGATATGAGCTCGGCA 441
Qy 362 GTATGAGATTGACAAACAGTTTGAAGACGCGCAAGAAATCAACAGATCGCTCTCCG 421
Db 442 AACTCTCTCTGACAAAGTCTTCCGGAACGGAGTCCCTGTAATGCCAGATTTGTGATG 501
Qy 422 CCTGATGAAGCCGCGCGGCTTGGGGTGTGAAGTCTTCCTGTTACGAATCAAGATT 481
Db 502 CCATCAACCAAGCTGTGACTGTGGGGTATCCGCTCTCTCCGTTATGATATCAAGGATA 561
Qy 482 TGGTTCGCGCGCAAGAAATCTTCCGCAATGCGAGCAAAATTAACCGCGGAAGCGGAA 541
Db 562 TCCATGTGCCACCCCGGGGTGAAGAGTCTATGACATGACAGGTGAGAGCGAGCGCGA 621
Qy 542 AACGCGCCGATATGCGGAATCCGAAGCGCGTAATAATCGAACAAATCAACTTGCATGTG 601
Db 622 AACGGGCCACAGTTTCTAGAGTCTGA-----GG 648
Qy 602 GTGAGCGTGAAGCCGAATCCAAATCCGAAGCGAGGCTCAGCGTGCCTCAATGCGT 661
Db 649 GACCCGAGAGTCCGCCATCATATGTGGCAGAGGAGGAGAAACAGGCCACAGTCTGGGCT 708
Qy 662 CCAATGCCGAGAAATGCGCGCATCAACGCGCCCAAGCGGAAGCGGAATCCTGGGCC 721
Db 709 CCGAAGCAGAAAGAGCTGAACAGATTAATCAGGACGAGAGAGGCGAGTGCAGTCTGG 768
Qy 722 TTGTTGCCGAAGCCATGCGCAAGCCATCCGTCAAATTGCGCGCGCCTTCAACCCAAAG 781
Db 769 CGAAGGCCAAGCTTAAGCTGAATTTGGAATCTTGCGCTGACGCTCTGACACAACTA 828
Qy 782 GCGGGGCGAGTGCAGTCAATCTGAAGATTGCGAACAATACGTAGCCGCTTCAACAATC 841
Db 829 ATGAGATGCGAGCAGCTTCACTGACTGTGGCGGAGATATGTGACGGCGTTTCCAAAC 888
Qy 842 TTGCCAAGAAGAAATACGCTGATTTATGCGCGCAATGTTCCGCAATGCGGAGCTCGA 901
Db 889 TGGCCAAAGACTCCAAACCTATCTACTGCTCCCTCCAAACCTGGGATGTCAACGACATGG 948
Qy 902 TTTCTGCGCGCATG 915
Db 949 TGGCTCAGGCCATG 962

RESULT 17
CR592181 1208 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0DC005YF20 of Neuroblastoma Cot
DEFINITION 25-normalized of Homo sapiens (human).
ACCESSION CR592181
VERSION CR592181.1 GI:50472988
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1208)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
Genoscope.
2 (bases 1 to 1208)
REFERENCE Direct Submission
AUTHORS Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
TITLE BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr
JOURNAL 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES

SOURCE

Location/Qualifiers

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/tissue_type="Neuroblastoma Cot 25-normalized"
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Query Match      16.4%; Score 155.6; DB 3; Length 1208;
Best Local Similarity 50.6%; Pred. No. 5.7e-35;
Matches 432; Conservative 0; Mismatches 389; Indels 33; Gaps 1;

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QY 62 TCATCCCCCAGAGAGATCCAGCTTGTGGAAGGCTGGGGCTTTCATGCGCCCTGA 121
DB 142 TCGTCCGACAGAGAGGCTGGGGTGTGGAGCAATGGCGATTCCAGCGGATCTGG 201
QY 122 CGGCGGTTTGAATTTTGAATCCCTTTATCGACCGGCTGCCCTACCGCCATTCGCTGA 181
DB 202 AGCGTGTTTGAATCTCTCACTCCCTGTGTAGACCGGATCGATATGTGCAGAGTCTCA 261
QY 182 AAGAAATCCCTTTAGACGTACCCAGCGGTGTGCATCAGCGGCGATATACGAATTGA 241
DB 262 AGGAATTTGTCAATCAAGCTGCTGAGCAGTGGCTGTGACTTTCGACATATTAATCTTGC 321
QY 242 CTGTTGACGCAATCATCTATTTCAGATTAACCGATCCGAATCTCGCTCATACGTTTGA 301
DB 322 AAATGATGAGATCTTTTACCTGCGCATCATGAGACCTTTACAGGCAAGCTACGTTGG 381
QY 302 GCAACTACATTATGAGCAATTAACCAAGCTTCCCAACGAGCTGGCTTCCGTTATCGGC 361
DB 382 AGGACCTGAGATACCTCTCACTCCAGCTAGCTCAAAACAACATGAGATCAGAGCTGGCA 441
QY 362 GTATGAGATTTGAGCAAAAGCTTTGAAGAACGGAAGAAATCAACAGTCCGCTCGC 421
DB 442 AACTCTCTCTGAGCAAAAGCTTTCGAGGAACGGGAAGTCCCTGATGCGACATTTGTGAT 501
QY 422 CCGTCAATGAAGCCCGCGGCTTGGGGTGTGAAAGTCCCTCCGTTACGAATCAAGAT 481
DB 502 CCATCAACCAAGCTGTGATCTGTGGGGTATCCGCTGCTCGTTATGATCAAGGATA 561
QY 482 TGGTTCGCGGCAAGAAATCTTTCGCGCATGAGGACAAATTAACCGCCGCAACCGGAA 541
DB 562 TCCATGTGCAACCCGCGGGAAGAGTATGCAATGCAAGTGGAGCGAGCGCGCA 621
QY 542 AACGCGCCGATTTGCGGAAATCCGAAGCGCGTAAATTCGAACAACTTGGCAATG 601
DB 622 AACGGGCCACAGTTCTAGAGTCTGA-----GG 648
QY 602 GTCAAGGTGAAGCCGGAATCCAAATCCGAAGGCGAGGCTGAGGCTGCGTCAATGCGT 661
DB 649 GGAACCCGAGAGTCCGCTCAATATGTGGCAAGAAAGGAAACAGGCGCCAGATCTGGCCT 708
QY 662 CCATATGCCGAGAAATTCGCCGATCAACCGCGCAAGGCGAAGCGAATCTTCGCGCC 721
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DB 769 CGAAGGCCAAGGCTAAGCTGAAGCTATTCGAATCTGTGCTGAGCTGACCAACATA 828
QY 782 GGGGGGCGATGCGGCAATCTGAAGATTGCGGGAACATATACGTAGCGGCTTCAACATC 841
DB 829 ATGGAATGCAAGAGCTTCACTGACTGTGGCGGAGCAATGTGACAGCGGCTTCCAAAC 888
QY 842 TTGCCAAGAAAGCAATAGCTGATTAATGCGCGCAATGTTCGCAATCGGAGCTTGA 901
DB 889 TGGCCAAAGAGCTCAACATATCTACTGCTTCAACCTGGGCGATGTACACGAGATG 948
QY 902 TTTTTCGCGCATG 915
DB 949 TGGCTCAGGCGCATG 962

```

RESULT 18

AF161458

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

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JOURNAL

MEDLINE

PUBMED

QY 242 CTGTTGACGCGATCATCTATTTCACAGTAACCGATCCCAACTCGCTTCATACGGTTGCA 301
 Db 274 AAATCGAATGAGAGTCTTACCTGCGCATCATGAGACCTTCAAGGCAAGCTTACGGTGG 333
 QY 302 GCAACTATATATGCGCATTAACCGAGCTTGGCCAAACGACCGTGCTTCGGTTATCGGGC 361
 Db 334 AGGACCTGAGTAGTCCGCTCAACCCAGCTAGCTCAAAACAACATGAGTCAAGAGCTCGGCA 393
 QY 362 GTATGAGATTGGACAAAACGTTTGAAAGACGCAAGAAATCAACATACGTCGCTCCG 421
 Db 394 AACTCTCTGAGCAAAAGTCTTCGGGAAACGGAGATCCCTGAATGCCAGCATTTGGATG 453
 QY 422 CCTTCGATGAAGCCGCGGGCTGGGGTGGAAAGTCTTCCTCGTTACGAAATCAAGATT 481
 Db 454 CCATCAACCAAGCTGCTGACTGTGGGTATCCGCTGCTCGTTATGAGATCAAGATGA 513
 QY 482 TGGTTCCGCGCGAAGAAATCTTGGCGGCAATGCAAGGCAAAATTAACGCCGACGCGGAA 541
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 QY 542 AACGCGCCGTAATTGCGCAATCCGAAGGCGGTAATAATGAACAATCAACCTTGCAAGTG 601
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 QY 602 GTCAAGCTGAAGCCGAAATCCAAATCCGAAGCGAGGCTCAGGCTGCGGTCAATGCGT 661
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 QY 662 CCAATGCCGAGAAATTCGCCCGCATCAACCGCGCAAGCGGAGGAGGCAATCCCTGCGCC 721
 Db 661 CGAAGCGAAGAAAGGCTAAACAGATTAATCAAGCGAGGAGGCGCAAGTCAAGTCTGG 720
 QY 722 TTGTTGCCGAAGCCATGCCGAAGCCATCCGTCAATTTGCGCGCCCTTCGAAACCCAG 781
 Db 721 CGAAGCGCAAGGCTTAAGCTTAAGCTATTCGATCTGCGTGCAGCTTGACACAGCTA 780
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 QY 842 TTGCGCAAGAAAGCAATTCGCTGATTAATGCCGCCAATGTTGCCGACATCGGACGCTGA 901
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 QY 902 TTTCTGCGCGCATG 915
 Db 901 TGGCTCAGGCGCATG 914

RESULT 19
 CR591719 1532 bp mRNA linear HTC 21-JUL-2004
 LOCUS full-length cDNA clone CSODK005YE05 of Hela cells Cot 25-normalized
 DEFINITION of Homo sapiens (human).
 ACCESSION CR591719
 VERSION CR591719.1 GI:50472526
 KEYWORDS HTC; CNSLT cDNA.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1532)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished
 Contact: Feng Liang Email: fliang@life.techn.com URL: <http://fulllength.invitrogen.com/>
 Faraday Avenue
 Genoscope.
 2 (bases 1 to 1532)
 REFERENCES
 AUTHORS Direct Submission
 TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
 JOURNAL BP 191 91006 Evry cedex - FRANCE (E-mail: sequef@genoscope.cns.fr)

COMMENT
 - Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.

FEATURES
 source
 Location/Qualifiers
 1..1532
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSODK005YE05"
 /tissue_type="Hela cells Cot 25-normalized"
 /plasmid="pCMVSPORT_6"

ORIGIN
 Query Match 16.4%; Score 155.6; DB: 3; Length 1532;
 Best Local Similarity 50.6%; Pred. No. 6.2e-35;
 Matches 432; Conservative 0; Mismatches 389; Indels 33; Gaps 1;

QY 62 TCATCCCCCAGAGAGATCCAGTTCGAAAGGCTCGGCGCTTCATGCGCCCTGA 121
 Db 141 TCGTCCGCGAGAGAGGCGCTGGGTGGAGCAATGGCCCATTCACCGATCCTGG 200
 QY 122 CGGCGGTTGAATATTTGATTCCTTTATCGACGCGCTGCTTACCGCATTCGCTGA 181
 Db 201 AGCTGGTTGAACATCCTCATCCTGTGTTAGACCGGATCCGATATGTGACAGATCTCA 260
 QY 182 AAGAAATCCCTTACGATGACGACGAGGCTGACATCAGCGGAGTAATACGAATGA 241
 Db 261 AGGAAATGTCATCAAGGCTGAGCAGTCGCTGACTGTGACATTCGACAAATGTAATCTGTC 320
 QY 242 CTGTTGACGCGATCATCTATTTCACAGTAACCGATCCCAACTCGCTTCATACGGTTGCA 301
 Db 321 AAATCGAATGAGTCTTACTCGGCAATGAGACCTTCAAGGCAAGCTACGGTGG 380
 QY 302 GCAACTATATATGCGCAATTAACGAGCTTGCCCAAGAGCGCTGCTTATCGGGC 361
 Db 381 AGGACCTGAGTATGCGGTCAACCCAGCTAGCTCAAAACAACATGATGAGAGCTCGCA 440
 QY 362 GTATGAGTTGACAAAACGTTTGAAGAAGCGCAAGAAATCAACATACGTCGCTCCG 421
 Db 441 AACTCTCTGAGCAAAAGTCTTCGGAGCGGAGTCTTGAAGCGCAGCATGTGTGATG 500
 QY 422 CCTCGATGAAGCCGCGGGCTTGGGGTGGAAAGTCTCCGTTACGAAATCAAGATT 481
 Db 501 CCATCAACCAAGCTGCTGACTGCTGGGTATCCGTCTCCGTTATGAGATCAAGATA 560
 QY 482 TGGTTCCGCGCAAGAAATCCTTCGCGCAATGACGAGCAAAATTAACCGCGAAGCGGAAA 541
 Db 561 TCCATGTGCCAACC CGGGGTGAAGAGTCTATGACAGTGAAGGACGAGCGGCGGA 620
 QY 542 AAGCGCGCGTATGTCGGAATCCGAAAGCGGTAAATCGAAACAATCAACTTGCAGTG 601
 Db 621 AACGGGCGCAAGTCTGAGTCTGA-----GG 647
 QY 602 GTCAAGCTGAAGCCGAATCCCAATCCGAAGGCGAGGCTCAGGCTGCGTCAATCGT 661
 Db 648 GAGCCCGAGAGTGGCCATCATATGTGGCAAGAGGAAAGAAACAGGCCCAATCTGGCCT 707
 QY 662 CCAATGCCGAGAAATGCGCGCATCAACCGCGCAAGGCGAAGCGAAATCCCTGCGCC 721
 Db 708 CCGAAGCAGAAAGCTGGAACAGATTAATACAGGACAGAGAGGCGAGTGCATCTGG 767
 QY 722 TTGTTGCCGAAGCCATGCGGAGGCTTCGTAATTTGCGCGCGCTTCAAAACCAAG 781
 Db 768 CGAAGCGCAAGGCTTAAGCTGAAGCTTTCGAATTCCTGCTGACGCTTACACAAACATA 827
 QY 782 GCGGGCGGATGCGGTCAATCTGAAGATTGCGGAAACAATACGTAGCCGCTTCAACAATC 841
 Db 828 ATGAGATGACAGAGCTTCACTGACTGTGCGGACGATATGTGAGCGGCTTCTCCAAAC 887
 QY 842 TTGCGCAAGAAAGCAATACGCTGATTAATGCGCGCAATGTTGCGGACATGGCAGCTGA 901

Db 888 TGGCCAGAGCTCCACACTATCTACTGCTCCACACCTGCGATGTACACAGCATG 947

Qy 902 TTTTGTCCCGGCATG 915

Db 948 TGGCTCAGGCGCATG 961

RESULT 20
BX400955 1023 bp mRNA linear EST 29-APR-2004
LOCUS BX400955 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
DEFINITION CDNA clone CS0DK0051E05 5-PRIME, mRNA sequence.
ACCESSION BX400955
VERSION BX400955.2 GI:46878596
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1023)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30626315.
CONTACT: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seque@genoscope.cns.fr; Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5178.r

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0DK005AC030Pic=5178.r.
Location/Qualifiers
1..1023
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DK0051E05"
/cell_line="HELA"
/cell_line="HELA"
/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 16.3%; Score 154.4; DB 5; Length 1023;
Best Local Similarity 49.0%; Pired. No. 1.3e-34; Indels 33; Gaps 1;
Matches 432; Conservative 13; Mismatches 404;

Qy 62 TCATCCCCCAGCAGAGTCCAGTGTGCGAAAGGCTCGGCGCTTTCATCGCGCCCTGA 121
|||
Db 141 TGTGTCGCGAGCAGAGGCTGTGCTGTGAGAGGATGGCGCATTCACCGGATCTCG 200
|||
Qy 122 CGGCGGTTGAATATTTGATTCCTTTATCGACCGGCTGACCGCATTCGCTGA 181
|||
Db 201 AGCTGTGTGAACATCTCATCTCTGTGTAGACCGGATCCGATATGTGCAAGTCTCA 260
|||
Qy 182 AAGAAATCCCTTAAAGAGTACCGACGAGGTGTCATCAAGCGGATATAGCAATTA 241
|||
Db 261 AGGAAATGTCTCAACAGTGTGAGAGAGTGGCTGTGATCTTGACAAATGTAACTCTG 320
|||
Qy 242 CTGTGACGCGCATCATCTATTTTCCAAATACCGATCCCAATCGGCTCATACGGTTCGA 301
|||
Db 321 AATGATGAGAGTCTTACCTGCGCATATGAGACCTTAAAGGCAAGTACGAGTGG 380
|||
Qy 302 GCAACTACATTAATGAGCAATTAACCAAGCTGCGCAAAAGACGCTGCTTATCGGGC 361

Db 381 AGAACCTGAGATGCTCCACCGAGCTAGCTCAAAACAACATGATCAAGCTCGGCA 440
|||
Qy 362 GTATGAGATTGACAAAACGTTTGAAGAACCGGACGAATCAACGATACCGTCTCG 421
|||
Db 441 AACTCTCTGTGACAAATCTTCGCGGAACGGAGATCCCTGATATCCAGCATTTGGATG 500
|||
Qy 422 CCTGTGATGAAGCGCGCGGCTTGGAGGTGTGAAGTCTCTCGTTACGAATCAAGATT 481
|||
Db 501 CCATCAACCAAGCTGTACTGCTGGGATATCCGCTGCTCGTTATGATGATCAAGATA 560
|||
Qy 482 TGGTTCGCGCGCAAGAAATCTTTCGCGCATGACAGGCAAAATTACCGCGGAACGGAAA 541
|||
Db 561 TCATATGTCCACCCCGGATGAAGAGTCTATGACAGATCGAGTGAAGGACGCGCGGA 620
|||
Qy 542 AACGCGCGCGTATTTGCCAATCCGAGAGCCGTTAAATGAACAAATCAACTTGCATG 601
|||
Db 621 AACGGGCCACAGTTCTAGATCTGA-----GG 647
|||
Qy 602 GTACAGCTGAAAGCCGAATTCACAAATCCGAAGGAGGCTCAGGCTGCGTCAATGCGT 661
|||
Db 648 GGACCCGAGAGTGGCCATCAATGTGCGAGAGGAGAAACAGGCCCAAGATCTGGCT 707
|||
Qy 662 CCAATGCCAGAAATCCCGCCGATCAACCGCGCAAGGCGAAGCGAATCCCTGCGCC 721
|||
Db 708 CCGAAGCAAAAGGCTGAACGATTAATCAGGAGGAGAGGCGAGTCAAGTTCG 767
|||
Qy 722 TTGTTCCGAGCAATGCGCGAAGGATCCGTAATTCGCGCGCCCTTCAAAACCCAG 781
|||
Db 768 CGAAGGCCAAGGCTAAAGCTGAAGCTATTCGATCTGCGACCTCTGACACAAACA 827
|||
Qy 782 GGGGGCGGATGCGGTCAATCGAAGATTGCGGAAATAGTAGCGGCTTCAACAATC 841
|||
Db 828 ATGAGATGACAGCACTTCACTGACTGTGGCCGACAGATATTCAGCGGTTCTCAAC 887
|||
Qy 842 TTGCCAAAGAAAGCAATAGCTGATTAATGCCGCAATGTTGCGCAATCGGACGCTGA 901
|||
Db 888 TGGCCAGAGGCTCCACACTATCTACTGCTCCACACCTGCGATGTACACAGCATG 947
|||

Qy 902 TTTTGTCCCGGCATGAAATTTATGACAGCAGCAAAACGCCCA 943
|||
Db 948 KGSITCAAGCCATGKGKTTATTGAGCCYCACCAARCCCMR 989
|||

RESULT 21
COS48169 906 bp mRNA linear EST 01-SEP-2004
LOCUS LYEST5061 Sea lamprey LyEST Petromyzon marinus cDNA, mRNA sequence.
DEFINITION COS48169
ACCESSION COS48169.1 GI:51796481
VERSION EST.
KEYWORDS Petromyzon marinus (sea lamprey)
SOURCE Petromyzon marinus
ORGANISM Petromyzon marinus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
1 (bases 1 to 906)
Pancer, Z., Meyer, W.E., Klein, J. and Cooper, M.D.
Proteolytic T-cell receptor and CD4-like coreceptor expressed in
lymphocytes of the aquanahan sea lamprey
Proc. Natl. Acad. Sci. U.S.A. 101, 13273-13278 (2004)
Contract: Pancer, Zeev
Division of Developmental and Clinical Immunology
The University of Alabama at Birmingham
378 Wallace Tumor Institute, 1530 Third Avenue, South, Birmingham,
AL 35294-3300
Tel: 205-975-5812
Fax: 205-975-7218
Email: zpancer@uab.edu
Location/Qualifiers
1..906
/organism="Petromyzon marinus"
/mol_type="mRNA"
/db_xref="taxon:7757"

/cell_type="lymphocyte"
/dev_stage="unstimulated larvae"
/clone.lib="Sea lamprey LYEST"
/note="Vector: lambda ZAP Express; lymphocyte mRNA ESTs
from unstimulated larvae. All are from arrayed colonies
from a directionally cloned cDNA library in lambda ZAP
Express (Stratagene). All are single pass 5' sequences."

ORIGIN

Query Match 16.2%; Score 153.4; DB 7; Length 906;
Best Local Similarity 50.8%; Pred. No. 2.4e-34;
Matches 367; Conservative 0; Mismatches 356; Indels 0; Gaps 0;

QY 48 CAAATCTTTGTCATCCCCCAGAGAAATCCACCTTTCGAAAGGCTCGGCGTTT 107
DB 166 CACGCGCGTGTGTTGTCGCCAGAGAGGCGGTGATCATCGAGCGCATGGAGCAT 225
QY 108 CCATCGCGCGCTGACGCGCGGTTGAATATTTGATTCCTTTATCGACCGCGTCCCTA 167
DB 226 CCACGCGCTACTCCGCGCGGTTGAATCTTGTATCCCGAATAATCGACAGATAAAGTA 285
QY 168 CCGCATTCGCTGAAGAATCCCTTGAAGTACCGACGAGCGTGCATCAGCGCGA 227
DB 286 CGTCAGAGCTTGAAGAATATGATCATGCACTTCCAGAGAGTCTGCATCACCCTGGA 345
QY 228 TAATACGCAATGACTGTTCAGCGCATCATCTATTTCCAAAGTAAACGATCCCAACTCGC 287
DB 346 TAAATGTTACACTGACACTGATGATGTGTGTGTAACCTCGCATTTATGACCCGTTCAAGGC 405
QY 288 CTATACGCTTCGAGCAATCAATTATGCAATTAACCACTTCGCGCAAGAGCGCTCGG 347
DB 406 GAGTACGCGCTCGAGAGACCCCGAGTACCGCGTACCGAGTGTCTGACACCATCCG 465
QY 348 TTCCGTTATCGGGGATGAGATTGAGCAAAACGTTTGAAGAAGCGCAAGTAATCAAG 407
DB 466 CTCGAGCTGAGCAAGATCGCGTGAACGCGTGTTAAGAGAGAGGTCTTGAAAGC 525
QY 408 TACCGTCTCTCCGCTTCATGAGAGCGCGCGCTTGGGGTGTGAAGTCTTCGTTA 467
DB 526 CAATCTGTGAGAGTAAATGAGGCGCGCGAGTATGGGGCATTCGTTGCTCCGCTA 585
QY 468 CGAAATCAAGATTTGTTCCGCGCAAGAAATCTTTCGCGCATGCAAGCAATTAAC 527
DB 586 CGAGTCAAGAGACATGAGCTGCTCAACCGCGTCAAGAGACCATGCGAGTGTGA 645
QY 528 CGCGAAGCGCAAAAGCGCGCGCTATTCGGAATCCGAGGCGGTAAATCGAACAAT 587
DB 646 GCGGAGCGCGCAAGCGAGCGGTGCTGAGAGTGGAGGCGCATTCGCGATCCGAT 705
QY 588 CAACCTTTCAGTGTGTCAGCTGAGAGCCGAATCCGAATCCGAGGCGAGGCTCAGGC 647
DB 706 CAACTGTGCGAGGCAAGAGCGCTCAACGATCTCGCTCGAGAGCTGAAGAGCGGA 765
QY 648 TCGCGTCAATGCTCAATGCGAGAAATGCGCGCATCAACCGCGCAAGAGCGGAAGC 707
DB 766 GCAGATCAACAGGAGGAGGCGCAAGCGTCCGCAATGTGAAGAAAGCATTCGCAAGGC 825
QY 708 GGAATCCCTGCGCGCTTGTTCGGAAGCGAATGCGGAACCATTCGTAATTTGCCGCGC 767
DB 826 GGAAGCCATCAAGCGCGCTGCAAGGCTCTCAAGAGCAAGCGCAACATGACGCGCTC 885
QY 768 CCT 770
DB 886 GCT 888

RESULT 22

CNS08NMD/c

LOCUS

DEFINITION

947 bp mRNA linear HTC 07-JAN-2003
Single read from an extremity of a full-length cDNA clone made from
Anopheles gambiae total adult females. 3-PRIME end of clone
FK0AA30AD01 of strain 6-9 of Anopheles gambiae (African malaria
mosquito).

ACCESSION BX020429
VERSION BX020429.1 GI:27569649
KEYWORDS HTC.
SOURCE Anopheles gambiae (African malaria mosquito)

ORANISM

Anopheles gambiae
Bukariyola; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Anopheles.

REFERENCE 1 (bases 1 to 947)

AUTHORS

Genoscope.

TITLE

Submitted (06-JUN-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqre@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

JOURNAL

location/Qualifiers

FEATURES

source

/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="6-9"
/db_xref="taxon:7165"
/clone="FK0AA30AD01"
/plasmid="pME18S-FL"
/note="end : 3-PRIME"

ORIGIN

Query Match 16.1%; Score 152.2; DB 3; Length 947;
Best Local Similarity 53.9%; Pred. No. 5.6e-34;
Matches 313; Conservative 0; Mismatches 268; Indels 0; Gaps 0;

QY 154 GACCGCTCGCTTACCGCCATTCGCTGAAGAATCCCTTTAGACGTACCAAGCAAGTGC 213
DB 947 GACCGGCTGAAGTACGTGAGAGTCTTGAAGAAATCCCAATAGACGTGCGAAACAGTCC 888
QY 214 TGATCAAGCGCGATTAATAGCAATGACTGTTAGACGAGCATCTATTTCGAATGTAAC 273
DB 887 GCATCAAGCTTCGCAACGTAAGCTCAGCATGACAGTGTGCTGTAACCTGCGATTCTC 828
QY 274 GATCCAAACTCGCTCATACGTTTCAGCAACTACTTAATGCAATTAACCAATTCAGCTTGGC 333
DB 827 GACCGTACTCGGTGCTGAGTGTGAGAGACCGGAGTTTGATCAACCAAGCTCGC 768
QY 334 CAACAGACGCTGCTTCCGTTATGCGCGTATGAGAGTTGACCAAAAGTTGAAGAACG 393
DB 767 CAACAGACGATGCGCTCGAGCTGCGCAAGATGCACTGACCAAGTGTCCGGAAGCGC 708
QY 394 GACGAATCAACAGTACCGTGTCTCGCCCTCGATGAGCGCGGAGCTTGGGGTGTG 453
DB 707 GAATCGCTCAACATCAGATCTGTGAGTTCATCAACAGCGAGCAAGCGTGGGATC 648
QY 454 AAAGTCTCGTTACGAATCAAGATTTGGTTCCGCGCAAGAAATCTTTCGCAATG 513
DB 647 TCTGTGCTGGGTACGAATCCGCGATCAAGCTGCGAGCGGGTGCAGAAAGCATG 588
QY 514 CAGGCAAAATTAACCGCGCAAGCGGAAAGCGCGCTATTCGCGAATCCGAAGCGCT 573
DB 587 CAGATGAGGTGAGGCGGAGCGCGCAAGCGGCGCGATCTCTGAGTGTGAGAGGTGTC 528
QY 574 AAATCGAACAATCAACTTTCGAGTGTGAGGCTGAGGCGGAATCCAAATTCGGA 633
DB 527 CGGCGGCGCATTTACGTGAGCGAGGAGGAGGAGGAGTGTGCGCATCTTGTCTCGAG 468
QY 634 GCGAGGCTCAGGCTGCGTCAATGCTTCAATGCGAGAAATGCGCGCATTCAGCGC 693
DB 467 GCGGAGAGGAGGAGGATCAATCGGCGATGTGAGGCGGCGCGCATCATGCGCTG 408
QY 694 GCCAAGGCGAAGCGGAATCCCTGCGCTTGTGCGCAAGC 734
DB 407 GCCGATGCGGTGCGAAAGTGTGAATGCTGCGCGCAATC 367

RESULT 23

CNI24718

LOCUS

847 bp mRNA linear EST 01-APR-2004

DEFINITION RHOH1_6_B03.g1.A002 Acid- and alkaline-treated roots Sorghum
bicolor cDNA clone RHOH1_6_B03_A002 5', mRNA sequence.
ACCESSION CN124718
VERSION CN124718.1 GI:45948467
KEYWORDS EST.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 847)
Cordonnier-Pratt M.-M., Suzuki Y., Sugano S., Klein R., Liang C.,
Sun F., Sullivan R., Lim S., Eastman A. and Pratt L.H.
An EST database from Sorghum: acid- and alkaline-treated roots
Unpublished (2003)
Other ESTs: RHOH1_6_B03.b1.A002
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Km. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Library constructed by Dr. Yuraka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & M University;
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
exclude polyA.
Seq primer: Sug5 (CTTCTGCTTAAAGCTGCG).
Location/Qualifiers
1..847
/organism="Sorghum bicolor"
/mol_type="mRNA"
/db_xref="taxon:4558"
/clone="RHOH1_6_B03_A002"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_1fb="Acid- and alkaline-treated roots"
/note="Organ: Root; Vector: pME18S-Fl3; Site_1: XhoI;
Site_2: XhoI; The library was prepared from polyA+ RNA
from 8-day-old roots harvested from Bix623 sorghum
seedlings grown in hydroponic culture. HCl was added to a
pH of 3.0 to some seedlings, KOH to a pH of 9.0 for
others. Roots were harvested 3, 12 and 27 hr after
addition and pooled for RNA preparation. Double-stranded
cDNA was cloned unidirectionally into different DraIII
sites of the pME18S-Fl3 vector (5-prime DraIII site is
CACTGTGTG, 3-prime DraIII site is CACCATGTG). XhoI excises
the cDNA insert."

ORIGIN

Query Match 16.0%; Score 151.4; DB 7; Length 847;
Best Local Similarity 55.4%; Pred. No. 9.4e-34;
Matches 293; Conservative 0; Mismatches 236; Indels 0; Gaps 0;

60 CGTCATCCCCCAGAGAGTCCAGTTGTCGAAAGCTCGGCGTTTCATCGCGCCCT 119
DB 297 CATAGTCCCGAAGAGGCTTTCGTCATCGAGAGTTGGAGATATTCAGAGCGCT 356
QY 120 GACGGCGGGTTGAATATTTGATTCCTTTATCGACCGCGTGCCTACCGCCATTGCT 179
DB 357 CGGCTCGGGTTCACTCTGTATCCCGCGCGGACCGATCGCTTAGTGAATCGCT 416
QY 180 GAAAGAAATCCCTTTAGACGTACCGACCGAGTGTGATACCGCGGATTAATCGCAAT 239
DB 417 CAAGGAGAGACCATCCCTCCCGACCAACCGCATCACCAAGAGCAACGTCAACAT 476
QY 240 GACTGTGACGGATCATATTTCCAGTAACGATCCCAAACTGCGCCATACGGTTC 299
DB 477 ACAGATGACAGCGCTATATGTCAAGATCAAGACCCCTTACTTCTTAAGGTGT 536

RESULT 24
CNS09K89
LOCUS
DEFINITION Single read from an extremity of a full-length cDNA clone made from
Anopheles gambiae total adult females. 5-PRIME end of clone
FK0AAC3CB04 of strain 6-9 of Anopheles gambiae (African malaria
mosquito).
ACCESSION BX062293
VERSION BX062293.1 GI:27635574
KEYWORDS HTC
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Anophelinae.
1 (bases 1 to 897)
REFERENCE
1. 897
Genoscope.
Direct Submision
Submitted (06-JAN-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Location/Qualifiers
1..897
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="6-9"
/db_xref="taxon:7165"
/clone="FK0AAC3CB04"
/plasmid="pME18S-Fl"
/note="end : 5-PRIME"

ORIGIN

Query Match 15.8%; Score 149.4; DB 3; Length 897;
Best Local Similarity 53.9%; Pred. No. 3.8e-33;
Matches 349; Conservative 0; Mismatches 296; Indels 2; Gaps 2;

65 TCCCCAGAGAGAGTCCAGTTGTCGAAAGCTCGGCGTTTCATCGCGCCCTGACGG 124
DB 252 TGCCCCAGAGAGAGATCGTGGAGCGATGGGCAAAATTTTACCGCATCTCGAGC 311
QY 125 CCGGTTGAATATTTGATTCCTTTATCGACCGCGTGCCTTACCGCATTTGCTGAAG 184
DB 312 CCGGCTGAAGCTCTGCTGCGCGGTGTGACCGGCTGAAGTACGTGACAGTCTGAAG 371
QY 185 AATTCCTTTAGACGTACCGACCGTGTGATACCGCGGATTAATGCAATGACGTG 244
DB 372 AATTCGCAATAGACGTGCGGAAACGTCCGCAATACGTCCGCAACGTAAAGCTACGA 431
QY 245 TTGACGGCATCATATTTTCCAGTAACCGATCCCAACTGCGCTCATACGGTTGAGCA 304
DB 432 TGAAGGTGTGCTGTACCTGCGGATTTCTGACCCGTAACCTCGGCTGTACGGTGTGAG 491

Oy		305	ACTACATTATGGAACAATTTCACAGCTGTGGCCAAACAGACGCTGGTTCGGTTATCGGGCGTA	364
Dd		492	AACCGGAAGTTTGCAATCACACCAGCTGCCCAAACGACCATGCCTCCAGACTGGGCAAGA	551
Oy		365	TGGAATTGGAACAAAAGTTTGAGAGAACGCGACGAATCAACAGTACCGTGTCTCCGCCC	424
Dd		552	TGTCACTGGAACAAAGGTGTTCCGGGAGCGCGAATCGCTCAACATCGATCGTAGTGAGTGA	611
Oy		425	TCGATGAAAGCCCGCGGGCTTGGGGTGTGAAAGTCTCCGTTACGAATCAAGAATTGG	484
Dd		612	TC-AACCAAGGCGAAGCAAGGAGGGGCATCTCTGTGCTCGGTACAAATTCGCGCATCA	670
Oy		485	TTCCGCCCCAAGAAATCTTGCGCGAATGACAGGCACAATTAACGCCGCAACGCGAAAC	544
Dd		671	AGCTGCCAGACCGGGTGCACGAAGGATGCAATGCAAGTGAAGCGGACGCG-CAAGC	729
Oy		545	GCGCCCGATTTGCGCAATTCGAAGGCGGTAAATCGAAACAATCAACTTGCCAGTGGTC	604
Dd		720	GGGCGCGATCCTCGAGTCGAGGGGTGTCCGGGCGCGCACTTAACGTGGCGCGAGGTA	789
Oy		605	AGCGTGAAGCGGAATTCACAAATCCGAAGGCGAGGCTCAGGCTGCGGTCAATGGTCCA	664
Dd		790	AGCGCAATTCGCGCATCTTGCTTCGAGGCGCAAGACGAGGAGATCAATCGGCGCA	849
Oy		665	ATGCCGAAAAATCGCCGCAATCAACCCGCCCAAGGCGGAAGCGGAA	711
Dd		850	ATGTGGAAGCGCGCCCATCATGAGGCGTGGCGCGAATCGCGTCCGAA	896
RESULT 25				
CB620196/c				
LOCUS	CB620196	657 bp	mRNA	linear EST 08-APR-2003
DEFINITION	OSIIeA05D17.r OSIIeA Oryza sativa (indica cultivar-group) cDNA			
ACCESSION	CB620196			
VERSION	CB620196.1	GI:29615183		
KEYWORDS	EST.			
SOURCE	Oryza sativa (indica cultivar-group)			
ORGANISM	Oryza sativa (indica cultivar-group)			
REFERENCE	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzaceae; Oryza.			
AUTHORS	Jantaasriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E., Kundna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.			
TITLE	Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe oryzae			
JOURNAL	Unpublished (2003)			
COMMENT	Contact: Rod Wing Arizona Genomics Institute University of Arizona Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ 85721-0088, USA Tel: 520 626 3967 Fax: 520 621 9288 Email: http://genome.arizona.edu			
FEATURES	PCR Primers FORWARD: gta aaa cga cgg cca gtg BACKWARD: gga aac agc tat gac cat g Plate: 05 row: D column: 17 Seq primer: gga aac agc tat gac cat g. Location/Qualifiers 1..657 /organism="Oryza sativa (indica cultivar-group)" /mol_type="mRNA" /cultivar="IR36" /db_xref="taxon:39946" /clone="OSIIeA05D17" /tissue_type="leaf" /dev_stage="3 week" /lab_host="DH10B" /clone_lib="OSIIeA"			

ORIGIN	Query Match	15.7%;	Score 148.8;	DB 6;	Length 657;
	Best Local Similarity	54.3%;	Pred. No. 5.2e-33;		
	Matches 300;	Conservative 0;	Mismatches 252;	Indels 0;	Gaps 0;
QY	60	CGTATCCCCAGAGAAATCCACGCTTGTGCAAAAGGCTGGGGGTTTCCATCGCGCCT	119		
Db	552	CATGTCGCCGAGAGAAAGAGGGTTCGGTGGAGACGGTTCGGCAAGTCAAGACGCT	493		
QY	120	GAGCGCGGGTTGAATATTTTGAATTCCTTATATGACCGGCGTCCCTACCGCATTCGCT	179		
Db	492	CGGCTCGGGATCCACGTCGTCGCCCTTCGTGACCGCATGCGCTTACGCTCACTGCT	433		
QY	180	GAAGAATAATCCCTTGAAGCGTACCAGCCAGGTCGATCACGCGCGATAATACGAATT	239		
Db	432	CAAGAGAGAGGCCATCCCATCCCGACAGTCGCGCATCACCAAGCAACGCTCCAT	373		
QY	240	GACTGTGACGGCATCATCTATTTCGAAGTACCGATCCCAATCGCTTCATACGGTTC	299		
Db	372	CCAGATGACGCGCGCTCTTACGTCGAAGATGTGTGATCCCTACCTTCCTTATGGGTGT	313		
QY	300	GAGCACTCACTTATGCGAATTAACCGAGTTCGCCCAACGACGCTGGGTTCCGTTATCG	359		
Db	312	GGAGATTCCAATTTTGTGATCATACAGCTTGCCCAACATCTATGAAAGTAGGCTTGG	253		
QY	360	GCGTATGAGTGTGACAAACGTTTGAAGAAGCGCAGAAATCAACAGTACCGTCTCTC	419		
Db	252	AAAGATTACCTTACACAAGACTTTTGAAGAGAGGATATCACTAATATGACAAATTTGTAG	193		
QY	420	CGCCCTGATGTAAGCCCGCGGGCTTGGGGTGTAAAGTCTCTCGTTACGAATTCAGGA	479		
Db	192	GTCATTATATGAGGCTCAACTGATGTGGGACGTGAATATGCTTACGTTATGATGATCAAGGA	133		
QY	480	TTTGGTTCGCGCGAAGAAATCCTTCGCGCAATGACAGACCAATTAACCGCGAAGCGGA	539		
Db	132	TATATCTCCGACAGTGGTGTAAAGTGCGCTATGAGATGCAACAGACGAAGAAAGGA	73		
QY	540	AAACGCGCCCGTATTCGCCGATCCGAAGCGCGTAAATCGAACAAATCACTTGGCAG	599		
Db	72	AAACGCTGCCAAATCCTTGATTCAGAAAGTGTATGTGATCATGTCAAAAGGCGCAAA	13		
QY	600	TGTCAGCGTGA	611		
Db	12	GGTGAGGCTGA	1		
RESULT 26	BM345666	623 bp	mRNA	linear	EST 23-JAN-2002
LOCUS	BM345666	623 bp	mRNA	linear	EST 23-JAN-2002
DEFINITION	rotochloensis cDNA 5'	similar to TR:Q9XVP9	Q9XVP9	F30A10.5	PROTEIN.
VERSION	BM345666	1	GI:18082581		
KEYWORDS	EST.				
SOURCE	Globodera rotochloensis				
ORGANISM	Globodera rotochloensis				
REFERENCE	1 (bases 1 to 623)				
AUTHORS	McCartner, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,				
	Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,				
	Bowers, Y., Gibbons, M., Ritzer, E., Bennett, J., Franklin, C.,				
	Tsagaris, I., R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,				
	Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,				
	Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,				
	McCann, R., Waterson, R., and Wilson, R.				
	The Washington Univ. Nematode EST Project, 1999				
TITLE	Unpublished (1999)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: McCartner JP				

The Washington Univ. Nematode EST Project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 The library was contributed by Dr. Geert Smant of the Laboratory of
 Nematology at Wageningen University, Wageningen,
 Netherlands (geert.smanthenema.dpw.wau.nl). DNA Sequencing by:
 Washington University Genome Sequencing Center
 Seq primer: -40RP from Gibco
 High quality sequence stop: 481.
 Location/Qualifiers

FEATURES

SOURCE

1. 623
 /organism="Globodera rostochiensis"
 /mol_type="mRNA"
 /db_xref="taxon:31243"
 /dev_stage="J2"
 /lab_host="DH10B"
 /clone_lib="Globodera rostochiensis U2 pCDNAT1 Smant v1"
 /note="Vector: pCDNAT1 (Invitrogen); Site 1: BstXI;
 Site 2: EcoRI; The library was donated for sequencing by
 Geert Smant from Wageningen University, Laboratory of
 Nematology, The Netherlands."

ORIGIN

Query Match 15.5%; Score 146.6; DB 4; Length 623;
 Best Local Similarity 53.6%; Pred. No. 2.3e-32;
 Matches 305; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

65 TCCCCAGAGAGATCCAGCTGTCGAAAGGCTGGGCTTCCATGCGCGCTGACGG 124
 55 TCCCCACAGATGCTGGGTTGTGACCGCGTGAATAATTCATCTTCTTACT 114
 125 CCGGTTGAATTTTGTATTCCTTATGACCGCGCTGCTACGCGCATTCGCTGAAG 184
 115 CCGGATGACATTTGTGACCGCTTCATGAGTATCGGTTATGACGACTGTGGAAG 174
 185 AATTCCTTTAGACGTAACCGACAGCTGTGATCAACGCGCGATTAATGCAATGACTG 244
 175 AGATGTCATGAAATTCCTCAAGAGAGCATGCAAGAGCAATGTCATGATGAT 234
 245 TTGACGGCATCATCTATTTCGAAAGTAAACGATCCCAACTCGCTCTATCGGTGAGA 304
 235 TGGATGCCATCTTATGTGCAAGTGTGACCCGTCACAGGCTTCTTACGAGCGCAAG 294
 305 ACTACATATGCGAATTAACCGAGCTTGCCCAACGACGCTGCTTATCGGCGCTA 364
 295 ATCCGGAATATGCGATTAATGTCAGCTGCAAAACCGTAATGGGTCCGAAGTTGGAAG 354
 365 TGGAGTTGACAAAAGTTGAAAGACGCGACGAATCAACATCCGTCCTCCGCC 424
 355 TGAATTTGATTAACGCTTCACAGAGCGGCAACTTAACATGGAATTTGTAAGGA 414
 425 TCGATGAAGCGCGCGGGGCTTGGGCTGTGAAGTCTCTCGTTACGAATTCAGATTTGG 484
 415 TCAAGGAATCCGCTTCAACATGGGCGCTAATTTGTTCTTACGAATTCGCAATATA 474
 485 TTCCGCGCGGAAGAAATCTTTCGCGCATGACGCAAAATTAACCGCGGAACGGAAAG 544
 475 ACATGCGACCGGAATTCAGCGGTGCATGAAATGCAAGTGAAGGCGAGCGAAAGAA 534
 545 GGGCGCGTATGCGCGAATCCGAAGCGCTGAATTAATTCGAACAAATCACTTGGCCAGTGC 604
 535 GTGCCGCAATTTTGAATCAGAGGCGATCTGCAAGCGGAGAAAGAACCGTGGAGG 594
 605 AGCGTGAAGCGGAATTCGAACATCCGAA 633
 595 AAAAGCAGGCTCGAATTTGCGCTCGAA 623

RESULT 27
 AL722012

LOCUS AL722012 712 bp mRNA linear EST 18-APR-2002
 DEFINITION AL722012 Danio rerio embryonic inner ear subtracted cDNA Danio
 rerio cDNA clone BNOA0572A10 3', mRNA sequence.
 ACCESSION AL722012
 VERSION AL722012.1 GI:20186616
 KEYWORDS EST.
 SOURCE Danio rerio (zebrafish)
 ORGANISM Danio rerio

REFERENCE
 AUTHORS 1 (bases 1 to 712)
 Coimbra, R., Weil, D., Brothier, P., Blanchard, S., Levi, M.,
 Hardelin, J.P., Weisenbach, J. and Petit, C.
 A subtracted cDNA library from the zebrafish (Danio rerio)
 embryonic inner ear

TITLE Unpublished (2002)

JOURNAL

Contact: Genoscope
 Genoscope - Centre National de Séquençage
 2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

SOURCE

1. 712
 /organism="Danio rerio"
 /mol_type="mRNA"
 /db_xref="taxon:7955"
 /clone="BNOA0572A10"
 /tissue_type="inner ear"
 /dev_stage="embryonic"
 /clone_lib="Danio rerio embryonic inner ear subtracted
 cDNA"
 /note="subtracted cDNA library"

ORIGIN

Query Match 15.3%; Score 145.4; DB 1; Length 712;
 Best Local Similarity 54.3%; Pred. No. 5.6e-32;
 Matches 287; Conservative 0; Mismatches 242; Indels 0; Gaps 0;

140 TGAATCCCTTATGCAACCGCGCTGCTACCGCATTCGCTGAAAGAAATCCCTTAGAG 199
 3 TCATCCGATCTTCACCGCGCTGCTGCAAGTGAACATGATGAGCAGGTGCTCGACA 62
 200 TACCGACGAGGTGTCATGACGCGCGCATTAATACCAATGCACTGTCAGCGCATCATCT 259
 63 TTCGGGCGAGGAATCATACCAAGACATGCAATGATGCTCCGGTCAATGGCGTCTCT 122
 260 ATTTCGAATTAACGATCCCAACTCGCTCTATGAGGCTTCAAGCACTAATTAATGCGAA 319
 123 TCTTCAGGTGCTCATGTCGCGCGCGCTTATGAGGTGACGACCTCTATCTTGGCA 182
 320 TTACCGAGTTCGCCAAGACGCTGCTGCTTATGAGGCTTATGAGTTGACCAAA 379
 183 TCATGAACCTGACGACACCACTCAANAACTGATGAGGCTGATGACCTGACGACA 242
 380 CGTTTGAAGAAAGCGACGAATCAACATGACGATGCTCGCGCTCGATGAAGCGCGC 439
 243 CGCTTTCGAAGCGACATATCAACGCGGCTGCTGCTGCTGATGACGAGCAACT 302
 440 GGGCTTGGGGTGAAGTCTTCGTTACGAATCAAGATTTGTTCCGCGCAAGAA 499
 303 CGCGCTGGGGGTGAAGATCAACCGGTGATCAAGATCAAGATCAAGATCAAGATCAAG 362
 500 TCTTCGCGCAATGACGACCAATTAATCCGCGAAGCGCAAAAGCGCGCTATATGCCG 559
 363 TTTTCGACCGCATGCGCGCGAGATGAAGCGCGCAAGCGCGCAAAAGCGCGCAATCTCG 422
 560 AATCGAAGCGCGTAAATCGAACAATCAACTGTCGATGATGATGATGATGATGATGAT 619
 423 AGCGGAAGCGATGCGCGCTCCAAATCTCTGCGCGCGAGGATGAAGAGCGCGCA 482
 620 TCCAAATATCCGAAGCGAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 668
 483 TCTGAGGCGCGAGGCGCGCGCGCGCGCGCTTCCGCGACCCNANAC 531

RESULT 28
CNS09090
LOCUS
DEFINITION
CNS09090 906 bp mRNA linear HTC 08-JAN-2003
Single read from an extremity of a full-length cDNA clone made from
Anopheles gambiae total adult females. 5-PRIME end of clone
FK0A07AC05 of strain 6-9 of Anopheles gambiae (African malaria
mosquito).
BX070122
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Anopheles gambiae (African malaria mosquito)
Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Anopheles.
1 (bases 1 to 906)
Genoscope.
Direct Submission
Submitted (06-JAN-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Location/Qualifiers
1. .906
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="6-9"
/db_xref="taxon:7165"
/clone="FK0A07AC05"
/plasmid="PM8185-FL"
/note="end : 5-PRIME"
ORIGIN
Query Match 15.3%; Score 145; DB 3; Length 906;
Best Local Similarity 54.5%; Pred. No. 7.9e-32;
Matches 332; Conservative 0; Mismatches 275; Indels 2; Gaps 2;
QY 65 TCCCCAGCAGGAAGTCACGTTGTCGAAAGGCTCGCGGCTTCCATCGCCCTGAGCG 124
DB 254 TGCCCCAGCAAGAGCATGATCGTGAACGATGCGCAAAATTTCACCGCATCTTCGAGC 313
QY 125 CCGGTTGAATATTGATTCCTTTATGACCGCGTGCGCTACCGCCATTG-CTGAAA 183
DB 314 CCGGCTGAACGTCCTGCTGCGCGGTGAGACCGGGTGAAGTACGTGACGAGGTCTGAA 373
QY 184 GAATCCCTTTAGACGTAACCAAGCGGTGTCATCAGCGCGATTAATGCCAATTGACT 243
DB 374 GAAATCGCAATAGACGTGCCAACAAGTCGCGCATCACTCCGACAGTAAAGCTCAGC 433
QY 244 GTGACGCGCATCATCTATTTCAGAGTAAACGATCCCAACTCGCCTCATAGGTTTCAGC 303
DB 434 ATCGAGGTGTGCTGTACCTCGCATTTCCAGCCGTAACCTCGGTGCTACGAGTGTGAG 493
QY 304 AACTACATTATGGAATTAACCAAGCTTGCCCAAGCAAGCTGCGTTATCGGCGT 363
DB 494 GACCCGAGTTTGCCATCAACCAAGCTGCGCAAGCAAGATGCGCTCGAGCTGGGCAAG 553
QY 364 ATGAGTTGGAACAAAGCTTTGAAGAGCGCAAGCAATCAACGATCGGTCTCCGCC 423
DB 554 ATGCACTGGAACAAGTGTTCGGGAGCGCAATCGCTCAACATCAGCATGTGGAGTGC 613
QY 424 CTCGATGAAGCGCGCGGGCTTGGGGTGTGAAGTCTCGGTTACGAATCAAGGATTTC 483
DB 614 ATCAACAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 673
QY 484 GTTCGCGCAAGAAATCTTCGCGCAATGACAGGCAAAATTACCGCGCAAGGAGGAGG 543
DB 674 AAGTCGCGAGCGCGGTGCAAGAGCGATGCAAGTGAAGTGAAGGAGGAGGAGGAGG 733
QY 544 CGCGCGGTATTCGCGAATCCGAAGCGGTAAATTCGAACAATCAACTTCGCGAGTGT 603
DB 734 GGGCGCGG-ATCTCTGATCGGAGGAGTGTCCGGCGCGCGCATTAAGTGGCGAGGAGT 792

RESULT 29
CD905963
LOCUS
DEFINITION
CD905963 780 bp mRNA linear EST 14-JUL-2003
mRNA sequence.
CD905963
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 780)
Genopiante.
Unpublished (2003)
Contact: Genopiante
Genopiante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genopiante' (<http://www.genopiante.com>
and <http://genopiante-info.infobiogen.fr>).
Location/Qualifiers
1. .780
/organism="Triticum aestivum"
/mol_type="mRNA"
/cullivar="rectal"
/db_xref="taxon:4565"
/clone="G468103H24"
/tissue_type="grain (468 degrees per day after
pollination)"
/clone_11b="G468"
ORIGIN
Query Match 15.3%; Score 144.6; DB 6; Length 780;
Best Local Similarity 53.2%; Pred. No. 9.9e-32;
Matches 306; Conservative 0; Mismatches 269; Indels 0; Gaps 0;
QY 60 CGTATCCCCCAGAGAGATCCACGTTTCGAAAGGCTCGGGCTTCCATCGCGCCT 119
DB 55 CATGTGCCGAGAGAGGCTTGTGATTAAGCGCTTCGGCAAGTACCTCAAGAGCT 114
QY 120 GACGCGGTTGATTAATTTGATTCCTTTATGACCGCGTGCCTACCGCCATTGCT 179
DB 115 GCACTCCGAGATCCAGGATCTGTCCTTCGTGACCGGATCGCATCGCATCTCT 174
QY 180 GAAAGAAATCCCTTTAAGACGTACCGACCAAGTCTGATCAACGCGCATTAATGCAATT 239
DB 175 CAAGAGAAAGACATCCCATCCCGACAGTCGCTATACCAAGATTAACGTGTCTAT 234
QY 240 GACTGTGAAGGATCATCTATTTCAGTAAGTACGATCCCAACTCGGCTCATAGGTTTC 299
DB 235 CCAATGACGCGCTCTCTTACGTAAGATGTTGATCCCTACGCTTCATATAGCGT 294
QY 300 GAGCACTACATTATGCAATTAACCGAGCTTGCCCAAGACAGCGTGCCTTCGTTATCGG 359
DB 295 GAGAAATCCATTTTTCAGTCACTTTCGAGTGAACAATATGAGTGAAGTGAAGTTCG 354
QY 360 GCGATGAGATTGACAAAAGTTTGAAGAACGAGCAAGAAATCAACGATACCGTGTCTC 419

DB 355 AAAGTAACCTTGGACAAAGACTTTTGAAGAGAGACACATTTGATGAGAAAGTGTGAG 414
QY 420 CGCCCTCATGAAAGCGCGGGCTTGGGGTGTGAAGTCTCCGTTACGAATCAAGA 479
DB 415 GTCCATAATGAGGCTTGACAGACTGGGGCTTGAAGTGTCTTCGTTATGAGATCAGGGA 474
QY 480 TTTGGTTCCCGCGCAAGAAATCTTCGGCAATGACGACAAATTAACCCCGCAACGGCA 539
DB 475 CATTTCTCTCCACCGGGCGTGAAGAAATGTAATGAGATGACGACGACGCAAGAGAG 534
QY 540 AAAAGCGCGCGGATTTGCGGAATTCGAAGCGCGTAAATCGAACAATCAACTTGCAG 599
DB 535 AAAGGTGCTCAATTTCTCACTCAGAAAGGGCTTATTTGATTCAGGACAAACCGGCAAA 594
QY 600 TGTGACGCGTGAAGCCGAAATCCAAATCCGAG 634
DB 595 GGGTGAAGGCTGAAGCGATCTCTCCAAATGACAAAG 629

RESULT 30
AY408617 1062 bp DNA linear GSS 15-DEC-2003
LOCUS Mus musculus STOML2 gene, VIRTUAL TRANSCRIPT, partial sequence,
ACCESSION AY408617.1 GI:39764588
VERSION AY408617.1 GI:39764588
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS 1 (bases 1 to 1062)
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B.,
Fertiera, S., Wang, G., Zheng, X.H., White, T.J., Snihsy, J.J.,
Adams, M.D. and Cargill, M.
TITLE Interfing nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1062)
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B.,
Fertiera, S., Wang, G., Zheng, X.H., White, T.J., Snihsy, J.J.,
Adams, M.D. and Cargill, M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source
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/db_xref="taxon:10090"
<1..>1062
/gene="STOML2"
/locus_tag="HMC3283"

ORIGIN
Query Match 15.3%; Score 144.6; DB 9; Length 1062;
Best Local Similarity 49.8%; Pred. No. 1.1e-31;
Matches 424; Conservative 0; Mismatches 394; Indels 33; Gaps 1;

QY 65 TCCCCAGAGAAAGTCACGTTTCGAAGAGTGGGGGTTTCATCGCGCCCTGACGG 124
DB 122 TCCCTCAGAGAGGCTGGGGTGTGACGAATGGCCGATTCACCGGATCTGGAAC 181
QY 125 CCGGTTGAATATTTGATTCCTTATCGACGCGCTGCTTACCGCATTCGCTGAAG 184
DB 182 CCGGCTGAAGCTCCGATCTCCCGTGTGACCGGATCCGATTCGAGAGAGCTCAAG 241
QY 185 AAATCCCTTGAAGCAGTACCGACGAGTGTGATCAAGCGGATTAATGCAATGATG 244

DB 242 AAATTGTTATCAAGTGCTGAGAGAGTGCAGCGTAACTCTTGACAAATGATTAACATCAAA 301
QY 245 TTGACGGCATCATATTTTCCAAAGTAAACGATCCAAACTGCCCTCATACGCTTGACA 304
DB 302 TAGATGAGTCCCTTATCTGCGCATCATGATCTCTTAACAGGCAAGTAAAGTGTGAAG 361
QY 305 ACTACATTAATGCAATTAACCGAGCTTGCCCAAGAGCGTGGTCCGTTATCGGGCGTA 364
DB 362 ACCGAGATGATGCTGTCAACCGATGAGTCTGACAGACATATGATCAAGAGCTTGCAAC 421
QY 365 TGAAGTTGACAAAACGTTTGAAGAACCGGACGAATCAAGTACCGTGTCTCCGCC 424
DB 422 TCTCTCTGACAAAGTTTTCGGAGCGTGAAGTCTTCAATGCCAAATTTGATGATGCA 481
QY 425 TCGATGAAGCGCGCGGCTTGGGGTGTGAAGTCTCTCGTTACGAATCAAGATTTGG 484
DB 482 TCAACCAAGCTGACAGATGCTGGGGTATCCGATGCTCGATCAAGATCAAGGACATCC 541
QY 485 TTCCGCGCGCAAGAAATCTTTCGCGCAATGACGACGAATTAACCGCGGACGCAAAAC 544
DB 542 ATGTGCACTTCGAGTGAAGAGTCTATGACAGTACAGTACAGGCAAGCGCCGAAAC 601
QY 545 GCGCCGTAATGCGCAATCCGAAAGGCGTAAATCGAACAATCAACTTGCAGTGTGTC 604
DB 602 GGGCCACAGTTCTAGAGTCCGA -----GGGA 628
QY 605 AGCGTGAAGCGGAATTCACAAATCCGAAAGCGGAGCTTCAGGCTGCGTCAATGCTCA 664
DB 629 CACGAGAGTCAAGCTTATATGTCGACAGAGGGAAMAAACAGCCCAAGTTCGCGCTCCG 688
QY 665 ATGCGGAGAAATGCGCGCGCATCAACCGCGCAAGGGAAGCGGAATCCCTGCGCTTG 724
DB 689 AAGCGAAAGAGCTGAACAGATTAATCAAGCGGCGGAGAGAGCCAGTCAAGTTTGCCA 748
QY 725 TTGCGGAAGCCATCCGAAAGCATCCGTAATTTGCGCGCGCTTCAACCAAGGCG 784
DB 749 AGCGCAAGCTTAAGCCGAAAGGATTCGAATTTCTGCGGCTGCTGATCAACATTAAG 808
QY 785 GGGCGGATGCGGTCAATGAAATTTGGGGAACAATGACGAGCGCGCTTCAACATTTTG 844
DB 809 GAGATGACGAGCTTCGCTCACTGTGGCTGAGCAGATATGTGACGCAATTTCCAAATCG 868
QY 845 CCAAGAAAGCATATCGCTGATTAATGCGCGCAATGTTGCGCATTCGCAACCTGATTT 904
DB 869 CCAAGGATTCACACAGTGTACGCTCCATTCACGACGACGATGATGTGG 928
QY 905 CTGCGCGCATG 915
DB 929 CTCAGGCGCATG 939

RESULT 31
AK002793 1536 bp mRNA linear HTC 03-APR-2004
LOCUS Mus musculus adult male kidney cDNA, RIKEN full-length enriched
DEFINITION library, clone:0610038f01 product:hypothetical protein, full insert
sequence.
ACCESSION AK002793
VERSION AK002793.1 GI:12833037
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Carninci, P. and Hayashizaki, Y.
JOURNAL High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itch,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL
MEDLINE
PUBMED
20493374
11042159

3
Shibata,K., Itch,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsumai,T., Tashiro,H., Itch,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamamoto,K., Matsunoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujisake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watabiki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuzura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multipillar sequencer
Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL
MEDLINE
PUBMED
20530913
11076861

4
The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

JOURNAL
REFERENCE
AUTHORS

5
The PANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

JOURNAL
REFERENCE
AUTHORS

6 (bases 1 to 1536)
Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,
Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,
Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,
Hirooka,T., Horii,P., Imotani,K., Ishii,Y., Itch,M., Izawa,M.,
Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,
Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C.,
Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
Shibata,K., Shibata,Y., Shingawa,A., Shiraki,T., Sogabe,Y.,
Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,
Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,
Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
Direct Submission

TITLE
JOURNAL

Submitted (10-JUL-2000) Yoshihide Hayashizaki. The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsunumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@sc.riken.jp,
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.jp/) for further
details.

COMMENT

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues. First strand cDNA was primed with a primer
[5' GAGAGGAGAGCGCGCACTGAGTGTGTTTTTTTTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse transcriptase
and subsequently enriched for full-length by cap-trapper. cDNA went
through one round of normalization to Rct = 5.0. Second strand cDNA
was prepared with the primer adapter of sequence[5'
GAGAGGAGAGGATCCAGAGCTCAATTATTATTAAATCAACCCCCCCC 3']. cDNA was
cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end:
XhoI. Host: SOLR.
location/Qualifiers
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/db_xref="PANTOM:DB:0610038F01"
/db_xref="taxon:10090"

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/clone="0610038F01"
/sex="male"
/tissue_type="kidney"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
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/note="unnamed protein product; hypothetical protein
(evidence: rscds,decoder,NCBI CDS Predictor,Longest-ORF)
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INQADQWGRICRYEIKDIHVPVRVSVMSQVARRRATVLTSEGTRESAINVA
EGKQKOITLASEKKAQINQQAAGSAVAKAKAKAEATRIITAGLTQNGDAASL
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1522..1527
polyA_signal
polyA_site
/note="putative"
1536
/note="putative"

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Best Local Similarity 49.8%; Pred. No. 1,2e-31;
Matches 424; Conservative 0; Mismatches 394; Indels 33; Gaps 1;
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polyA_site
/note="putative"
1536
/note="putative"

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125 CCGGTTGAATATTGATTCCTTATCGACCGCGTCGCTACCGCATTCGCTGAAG 184
190 CGGCGCTGAACGCTCTGATCCCGTGTGAACCGAATCCGATAGTGCAGAGTCTCAAG 249
185 AATCCCTTGAAGCTACCGCAGCGAGCTGATCAGCGCGATATATACGAATGACTG 244
250 AATATTGATTCACGCTGCTGAGAGTACGACCGTATCTTGAACATGTAACATACAA 309
245 TTGACGCGATCATCTATTTCGAATACGAATCCGATCCCAATCGCTCATACGTTGACGA 304
310 TAGATGAGTCTTATCTGCGCATCATGATCTCTTCAAGGCAAGTACGATGTGGAAG 369
305 ACTACATTATGCGAATTAACCAAGCTTGCCTGCAAGAGCGTCCGTTATCGGAGTA 364
370 ACCGAGATGATCTGTACCCAGTGAAGTCAAGACGACTATGAGTCAAGAGCTTGGCAAAAC 429
365 TGAAGTTGACAAACGTTTGAAGAACGACGCAAGCAATCAACATGACCGTCTCCGCC 424
430 TCTCTCTGACAAAGTTTTCGGAAGGCTGAGTCTCGAATGCCAATGTGTGATGCCA 489
425 TCGATGAAGCGCGCGGCTTGGGGTGTGAAGTCTTCCTGTTACGAATCAAGATTGG 484
490 TCAACCAAGCTGACGATGCTGGGTATCCGATCTCGCATACGAATCAAGACATTC 549
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545 GCGCGCTATTTGCGAATTCGAAAGCGTAAATTCGAACAAATCAACTTGCAGTGTGC 604
610 GGGGCAAGTTCTAGAGTCCGAA-----GGGA 636
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637 CAGGAGAGTGAATTAATGTGGCAGAGGGGAAGAAAGAGCCCAATCTTGCCCTCG 696
665 ATGCGGAAATATGCGCGCATCAACCGCGCAAGGCGAAGCGGAATCCTTGCGCTTG 724
697 AAGCAGAAAAGCTGAACAGATTAATCAAGCGCGCAGGAAGCAAGTGCAGTTCTGCGCA 756

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QY	725	TTGGCGAAGCAAGCCGGAAGCCATCCGTAAATTTGGCGCGCCCTTCAAAACCAAGGCG	784					
Db	757	AGCGCAAGGCTAAAGCCGGAAGCCATTCGAATTTCTGGCTGGGGCTCTGACATCAATATG	816					
QY	785	GGGCGGATGCGGTCATCTGATAGATTGCGGAACATATCGTAGCCGCGTTCAACATCTTG	844					
Db	817	GAGATGACAGACGCTTCGCTCACTGTGGCTGAGCAGTATGTGAGGGCAATTTCCAAATCGG	876					
QY	845	CCAAAGAAAGCATATCGCTGATTATGCCCGCCATATGTTGCCGACATGGCAGCTGATTT	904					
Db	877	CCAAGGATTTCAACACAGCTGACTAGCTCCCTTCAATCCAGCAGCATGACGATATGTGTGG	936					
QY	905	CTGCCCGGATG 915						
Db	937	CTCAGGCCATG 947						
RESULT 32								
LOCUS	BOS79084	705 bp	mRNA	linear	EST 19-JUN-2002			
DEFINITION	WHR2965_C05_F09GS Wheat dormant embryo CDNA library Triticum aestivum CDNA clone WHR2965_C05_F09, mRNA sequence.							
ACCESSION	BOS79084							
VERSION	BOS79084.1	GI:21482401						
KEYWORDS	EST.							
SOURCE	Triticum aestivum (bread wheat)							
ORGANISM	Triticum aestivum							
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.							
AUTHORS	1 (bases 1 to 705) Anderson,O.D., Chao,S., Chin,A., Close,T.J., Doherty,L., Fenton,R.D., Lazo,G.R., Rausch,C.J., Walker-Simmons,M.K. and Wilson,C.							
TITLE	The structure and function of the expressed portion of the wheat genomes - Dormant embryo CDNA library							
JOURNAL	Unpublished (2001)							
COMMENT	Contact: Olin Anderson US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA Tel: 5105595773 Fax: 5105595818 Email: oanderson@pw.usda.gov Sequences have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: SK primer.							
FEATURES	Location/Qualifiers							
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	/cultivar="Brevor"							
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	/clone="WHR2965_C05_F09"							
	/tissue_type="Seed embryo"							
	/dev_stage="Mature seed"							
	/lab_host="E. coli SOLR"							
	/clone_lib="Wheat dormant embryo CDNA library"							
	/note="Vector: Lambda uni-zap XR, excised phagemid; Site 1: EcoRI; Site 2: XhoI; Plants were grown to seed maturity under conditions favoring seed dormancy (L. Doherty at K. Walker-Simmons lab, Washington State University, Pullman, WA). Embryos were cut from mature dormant seed (Doherty). Total RNA was prepared from these embryos, polyA was purified, a cDNA library was made, and the cDNA clones were in vivo excised to give plus-script phagemids in the T7 close lab at the University of California, Riverside (Chin, Fenton). Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."							

	Best Local Similarity	53.5%	Pred. No. 5e-31;	
	Matches	297;	Conservative	0;
			Mismatches	258;
			Indels	0;
			Gaps	0;
QY	60	CGTCATCCCGACGAGGAGTCCACGTTGTCGAAAGGCTCGGGCGTTTCATCGCGCCT	119	
Db	22	CATGTCGCCGAGAGGAGGCTTCGTGATTGAGCCCTTCGGCAAGTATCTCAAGACCT	81	
QY	120	GACGGCCGGTTTGAAATTTTGTGATTCCCTTATGACCGCGTGCCTTACCGCCATTGCT	179	
Db	82	CGACTCCGGAGTCACGGGCTCGCCCCCTCGTGTGACCGGATCGCTCAAGCATCTCT	141	
QY	180	GAAGAAGATCCCTTAAACGTACCCACGACGTCGTGATCAACGGCGATTAATAGCAATT	239	
Db	142	CAAGAGAGAGACCATCCCATCCCGACGATCCGCTATCACCAAGATTAAGTGTGAT	201	
QY	240	GACTGTTAGCGGCATCATATTCTTCAAGTAAACCGATCCAACTGCTCATACGTTTC	299	
Db	202	CCAAATGAGAGGCGCTCCTTAACGTCAAGATTGTGATCCCTACCGTCTTCATATGGCGT	261	
QY	300	GAGCACTACATTATGCAATTACCGACTTGGCCCAACGACGCTGGCTTCGTTATCGG	359	
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QY	360	GCGATGAGATTGGACAAAACGTTTGAAGAACGGACGAAATCAACAGTACCGTCTTC	419	
Db	322	AAAGTAACTCTTGACAAAGACTTTTGAAGAGAGGAGACATGATGAAAGATTGTGAG	381	
QY	420	CGCCCTCGATGAGCCCGCGGGCTTGGGGTGTGAAGTCTCCGTTACGAAATCAAGA	479	
Db	382	GTCATTAATAGAGCTTCGACAGACTGGGGCTTTAAGTGTCTTGTTATGAGATCTAGGA	441	
QY	480	TTTGTTCCCGCGGACAAAGATCTTTCGGGCATGACGAGCAAAATTACCGCGCAACGCGA	539	
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QY	540	AAAAACGCGCCGTAATTGCCGAATCCGAAGCCGTAATAATGAAACAATCAACTTGGCAG	599	
Db	502	AAAGCGTGCTCAAAATTCCTCAAGACGAAGAGGGCTATGTTGATCAGGCAAAACCGGCCAA	561	
QY	600	TGTCACGCTGAAGC	614	
Db	562	GCGTAGGCTAAGC	576	

RESULT 33
 BM423347
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 ORGANISM
 SOURCE
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

BM423347 1095 bp mRNA linear EST 29-JAN-2002
 AGENCOURT 6402181 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5516467
 5', mRNA sequence.
 BM423347
 BM423347.1 GI:18391559
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 1095)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: DCTD/DRP
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Place: LNCM2017 row: b column: 20
 High quality sequence stop: 503.
 Location/Qualifiers
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 41"
/notes="Organ: skin; Vector: pORF7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
ORIGIN
Query Match      15.0%; Score 142; DB 4; Length 1095;
Best Local Similarity 50.1%; Pred. No. 6.6e-31;
Matches 410; Conservative 0; Mismatches 375; Indels 33; Gaps 1;

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3 GTGGTGAGCGAATGGCGCAATCCAGATCCCGAGCTGTGAAAGCTGTTGAACATCTCATC 62
145 CCTTTATGACCGCGGTGCGCTACCGCCATTGCTGAAAGAAATCCCTTTAGACGTACC 204
63 CTTGTGTTAGACCGGATCGATATGTGAGAGCTTCAGAGAAATTTGATCATCAGTGTCT 122
205 AGCCAGCTCTGCATCACCGCGATTAATAGCAATGACTGTGACGCGCATCTATTTC 264
123 GAGGAGTGGGTGTGACTCTGCAATGTAATCTGCAAAATGATGAGATCCTTTACTTG 182
265 CAAGTACCGATCCCAAACTGCTCATACGTTTGACCACTACATTAATGCAATTACC 324
183 CGCATCATGAGACCTTTAAGAGCACTACGTTGAGAGAGCCCTGAGTATGCCGTACC 242
325 CAGCTTGCCCAAGACGCGCTGCTCGTTATCGGCGCTATGAGAGTGAACAAACGTTT 384
243 CAGCTAGCTCAAAACACATGATGATCAAGCTCGGCAAACTCTCTGTGACAAAGTCTTC 302
385 GAAAGAACGCAAGCAATCAAGTACCGTCTCTCCGCTCGATGAAAGCGCGGGGCT 444
303 CGGGAACGGAGTCCCTGAAATGCGAGATTTGATGTCATCAACAGATGCTGACTGC 362
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363 TGGGGTATCCCGCTGCTCCGTTATGAGATCAAGATATCCATGTGCCACCCGGGTGAA 422
505 CGCGCAATGCAAGCAAAATTAACGCGCAAGCGGCGCCGATTTGCCAATCC 564
423 GAGTATATGCAATGCAAGTGAAGCAAGCGCGGAAACGGGCGCAAGTCTTAGAGTCT 482
565 GAAAGCCGTAAATGCAAAATCAACTTGCAGTGTGTCAGCGTGAAGCGGAAATCCAA 624
483 GA-----GGGGAACCGGAGTCCGCCATCAT 509
625 CAATCCGAAGCGAGGCTCAGGCTCGGTCAATGCTCAATCCGAGAAATGCCCCGC 684
510 GTGGCAAGAGGAAACAAAGGCCAGATCTGTGGCTCCGAAAGCAAGAAAGCTGAACAG 569
685 ATCAACCGCGCAAGCGGAAAGCGGATCCCTGCGCTTGTGGCGGAAGCAATCCGAA 744
570 ATTAATTCAGCGACGAGAGAGGCCAGTCAAGTTCTGGGAAAGGCCAAGCTTAAGCTGAA 629
745 GCATTCCTCAAAATTTGCGCGCCCTTCAAAACCAAGCGGGCGAGTCCGTCATCTG 804
630 GCTATTTGAATCTTGCTGACGCTCTGACAAACAATAATGAGATGACAGCTTCACTG 689
805 AAGATTTGGAACATATGTAAGCGCTTCAACAACTTTGCCAAGAAAGCAATTCGCTG 864
690 ACTGTGCGGAGAGTATGTCAACGCTTCTCAAACTGGCGCAAGGACTCCAAACATATC 749

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Cy      865 ATTATGCCCGCAATGTTCCGACATCGGACCTGAT 902
Db      750 CTACTGCCCTTCACACCTGGGAGATGTCACCAAGATGTT 787

RESULT 34
LOCUS   COS32841
DEFINITION 3530 bp mRNA linear EST 15-JUL-2004
INVOG 1216.1 B02.Y.1 3530 - Full length cDNA library created by
ACCESSION INVITROGEN from multiple tissues Zea mays cDNA, mRNA sequence.
VERSION   COS32841
KEYWORDS  GI:50337715
SOURCE    EST.
ORGANISM  Zea mays
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           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
           clade; Panicoideae; Andropogoneae; Zea.
           1 (bases 1 to 648)
           Walbot, V.
           Maize ESTs from various cDNA libraries sequenced at Stanford
           University
           Unpublished (1999)
           Contact: Walbot V
           Department of Biological Sciences
           Stanford University
           855 California Ave, Palo Alto, CA 94304, USA
           Tel: 650 723 2227
           Fax: 650 723 8221
           Email: walbot@stanford.edu
           Plate: 3530.1 216.1 row: B
           Location/Qualifiers
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               Project contracted with Invitrogen to produce a
               normalized, full length library in a pSport vector. This
               is a Gateway compatible vector, permitting clone movement
               to new vector backbones for expression in diverse host
               cells using recombination rather than restriction enzymes.
               Details of the vector and sequencing primers are available
               at ZmDB in the EST library description tables. poly(A)+
               mRNA was prepared by Invitrogen, and equimolar amounts of
               RNA from each of the 12 tissue samples were mixed together
               for selection of mRNA with a 5' cap. After synthesis of
               cDNA, a normalization step was conducted against the
               mixture of RNA sources. This step effected a 20X to 80X
               reduction in common transcript types. Tissues prepared: 1.
               just emerging silks; 2. inner husks from ears of sample
               #1; 3. 20 day aleurone; 4. Immature tassels; stages from
               1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm
               vegetative shoot tips from 15 day old seedlings; all
               leaves with an expanded or partially expanded sheath
               were removed; 8. mature leaf tissue; 9. 0.5 cm long root
               tips from 15 day old seedlings; 10. 10 day whole seed; 11.
               12 day endosperm and embryo; 12. 17 day endosperm and
               embryo. All of the sequenced clones in project 3530 will
               be archived at the University of Arizona along with the
               unigene clones from the Maize Gene Discovery EST
               sequencing projects. Clones can be ordered through the
               ZmDB web site or directly from the University of Arizona
               (http://www.genome.arizona.edu/orders/). High density
               filters containing over 18,000 clones can also be ordered

```

ORIGIN from the University of Arizona."

Query Match 15.0%; Score 141.8; DB 7; Length 648;
Best Local Similarity 54.8%; Pred. No. 6.5e-31;
Matches 281; Conservative 0; Mismatches 232; Indels 0; Gaps 0;

125 CCGGTTTGAATTTTGGATTCCTTATGACCGCGCTGACCGCATTAATGCAATGACTG 244
DB CCGGTTTGAATTTTGGATTCCTTATGACCGCGCTGACCGCATTAATGCAATGACTG 244
6 CCGGTTTGAATTTTGGATTCCTTATGACCGCGCTGACCGCATTAATGCAATGACTG 244
185 AAATCCCTTGAACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 244
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66 AAATCCCTTGAACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 244
DB AAATCCCTTGAACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 244
245 TTGACGCGATCATCTATTTTCAAGTAACCGATCCCAACTGCGCTCATACGCTTGAAGA 304
DB TTGACGCGATCATCTATTTTCAAGTAACCGATCCCAACTGCGCTCATACGCTTGAAGA 304
126 TTGACGCGATCATCTATTTTCAAGTAACCGATCCCAACTGCGCTCATACGCTTGAAGA 304
DB TTGACGCGATCATCTATTTTCAAGTAACCGATCCCAACTGCGCTCATACGCTTGAAGA 304
305 ACTACATTAATGCAATTAACCGACGCTGCGCAACGACGCTGCGCTGCGCTGCGCTGCG 364
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186 ATCCATATCTATCTGCTCTACCACTTGCACAAACCAACATGAGAGTGAACCTGCGGAGA 245
DB ATCCATATCTATCTGCTCTACCACTTGCACAAACCAACATGAGAGTGAACCTGCGGAGA 245
365 TGGAGTTGAGCAAAACGTTTGAAGAACGAGCAAAATCAACAGTACCGCTGCTCGGCC 424
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246 TTAACCTTGAATTAAGTCTTGAAGAACGAGCAAAATCAACAGTACCGCTGCTCGGCC 424
DB TTAACCTTGAATTAAGTCTTGAAGAACGAGCAAAATCAACAGTACCGCTGCTCGGCC 424
425 TCGATGAAGCCGCGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 484
DB TCGATGAAGCCGCGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 484
306 TCAATGAAGCCGCGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 484
DB TCAATGAAGCCGCGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 484
485 TTCCGCGCGCAAGAAATCTTGGCGCAATGAGGCGCAAAATCAACAGTACCGCTGCTCGGCC 544
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366 ATCTCTCAACGAGGATTAAGGAGGCTATGAGATGAGGAGGCTGAGGAGGAGGAGGAGG 425
DB ATCTCTCAACGAGGATTAAGGAGGCTATGAGATGAGGAGGCTGAGGAGGAGGAGGAGG 425
545 GGGCGCGCTATTTGCGCAATTCGGAAGCGCGCAAAATCAACAGTACCGCTGCTCGGCC 604
DB GGGCGCGCTATTTGCGCAATTCGGAAGCGCGCAAAATCAACAGTACCGCTGCTCGGCC 604
426 GGGCGCGCTATTTGCGCAATTCGGAAGCGCGCAAAATCAACAGTACCGCTGCTCGGCC 604
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605 AGCGTGAAGCCGCAAAATCAACATCCGAGGCG 637
DB AGCGTGAAGCCGCAAAATCAACATCCGAGGCG 637
486 AAAAGACTGCCAGATCTTGAATCTGAAGAG 518

RESULT 35
LOCUS CO010421 967 bp mRNA linear EST 09-JUN-2004
DEFINITION EST798756 Coccidioides posadasii spherule cDNA library, 0.4 to 2.3
kb Coccidioides posadasii cDNA clone CIEBH47 5' end, mRNA sequence.

ACCESSION CO010421
VERSION CO010421.1 GI:48517310
KEYWORDS EST.
SOURCE Coccidioides posadasii
ORGANISM Coccidioides posadasii
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.

REFERENCE 1 (bases 1 to 967)
AUTHORS Gardner M.J. and Cole G.T.
TITLE Analysis of gene expression in Coccidioides posadasii mycelia and
spherules via expressed sequence tags
JOURNAL Unpublished (2003)
COMMENT Other ESTs: EST798755
Contact: Gardner MJ
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org
Seq primer: M13 Reverse.
Location/Qualifiers
1. 967
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/note="Vector: pExpress 1; Site 1: Not I; Site 2: Eco RV;
Coccidioides posadasii spherule cDNA library, 0.4 to 2.3
kb"

ORIGIN
Query Match 14.9%; Score 141.6; DB 7; Length 967;
Best Local Similarity 53.0%; Pred. No. 8.4e-31;
Matches 303; Conservative 0; Mismatches 265; Indels 0; Gaps 0;

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DB CCGGTTTGAATTTTGGATTCCTTATGACCGCGCTGACCGCATTAATGCAATGACTG 184
369 CCGGATTTGCGCATTTCTGATGCGCTTATGACCGGATTTGCTGATGAAAGCTTGAAG 428
DB CCGGATTTGCGCATTTCTGATGCGCTTATGACCGGATTTGCTGATGAAAGCTTGAAG 428
185 AAATCCCTTGAACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 244
DB AAATCCCTTGAACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 244
429 AAGTGGCGATGATTAACCAATGCAATGCTATACGACGATTAACGATGACGCTGAGC 488
DB AAGTGGCGATGATTAACCAATGCAATGCTATACGACGATTAACGATGACGCTGAGC 488
245 TTGACGCGATCATCTATTTTCAAGTAACCGATCCCAACTGCGCTCATACGCTTGAAGA 304
DB TTGACGCGATCATCTATTTTCAAGTAACCGATCCCAACTGCGCTCATACGCTTGAAGA 304
489 TGGAGTTGAGCAAAACGTTTGAAGAACGAGCAAAATCAACAGTACCGCTGCTCGGCC 548
DB TGGAGTTGAGCAAAACGTTTGAAGAACGAGCAAAATCAACAGTACCGCTGCTCGGCC 548
305 ACTACATTAATGCAATTAACCGACGCTGCGCAACGACGCTGCGCTGCGCTGCGCTGCG 364
DB ACTACATTAATGCAATTAACCGACGCTGCGCAACGACGCTGCGCTGCGCTGCGCTGCG 364
549 AGCGCAATTAACCGCAATTTCTCAATTTGCGCCACACCAATGAGTTCGGAATTTGGCAGC 608
DB AGCGCAATTAACCGCAATTTCTCAATTTGCGCCACACCAATGAGTTCGGAATTTGGCAGC 608
365 TGGAGTTGAGCAAAACGTTTGAAGAACGAGCAAAATCAACAGTACCGCTGCTCGGCC 424
DB TGGAGTTGAGCAAAACGTTTGAAGAACGAGCAAAATCAACAGTACCGCTGCTCGGCC 424
609 TCACTTGAACGACGCTCTTAAAGAACGCTAATCTTAATGCAATTTTCTCAAGCA 668
DB TCACTTGAACGACGCTCTTAAAGAACGCTAATCTTAATGCAATTTTCTCAAGCA 668
425 TCGATGAAGCCGCGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 484
DB TCGATGAAGCCGCGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 484
669 TCAAGGAGGCGCGCGAGGATTTGGGCGGTGATGCTTGTGTTACGAAATTAAGATATCC 728
DB TCAAGGAGGCGCGCGAGGATTTGGGCGGTGATGCTTGTGTTACGAAATTAAGATATCC 728
485 TTCCGCGCGCAAGAAATCTTGGCGCAATGAGGCGCAAAATCAACAGTACCGCTGCTCGGCC 544
DB TTCCGCGCGCAAGAAATCTTGGCGCAATGAGGCGCAAAATCAACAGTACCGCTGCTCGGCC 544
729 ATGCTCTGAAGAGATGTTGGCGGCTATGCAATGCTCAACGCAAAATCAACAGTACCG 788
DB ATGCTCTGAAGAGATGTTGGCGGCTATGCAATGCTCAACGCAAAATCAACAGTACCG 788
545 GGGCGCGCTATTTGCGCAATTCGGAAGCGCGCAAAATCAACAGTACCGCTGCTCGGCC 604
DB GGGCGCGCTATTTGCGCAATTCGGAAGCGCGCAAAATCAACAGTACCGCTGCTCGGCC 604
789 GAGCTGATATTTTGAATCTGAAGGTCAGAGACGAGCGCAATCAATCGAGAGGATC 848
DB GAGCTGATATTTTGAATCTGAAGGTCAGAGACGAGCGCAATCAATCGAGAGGATC 848
605 AGCGTGAAGCCGCAAAATCAACATCCGAGGCG 636
DB AGCGTGAAGCCGCAAAATCAACATCCGAGGCG 636
849 GGAACATTCGATCTTGGCTCCGAGGCC 880

RESULT 36
LOCUS BF263774 814 bp mRNA linear EST 23-OCT-2001
DEFINITION BF263774 HV_CBA007K04f Hordeum vulgare seedling green leaf EST library,
cDNA clone HV_CBA007K04f, mRNA sequence.
ACCESSION BF263774
VERSION BF263774.2 GI:13261063
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticaceae; Hordeum.
REFERENCE 1 (bases 1 to 814)
AUTHORS Wing, R., Close, T.J., Kleinof, A., Wise, R., Wei, F., Begum, D.,

TITLE

Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton, R.D., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource for barley genomics: Blumeria infected incompatible (M1a13) seedling leaf cDNA library

JOURNAL COMMENT

Unpublished (2001)
On Nov 17, 2000 this sequence version replaced gi:11194768.
Contact: Ming RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 590
Seq primer: AATTACCTCCTACTAAGG
High quality sequence stop: 755.
Location/Qualifiers

FEATURES

source

1. 814
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="C116155 (M1a13)"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="HV_CEA007K04f"
/tissue_type="seedling green leaf"
/lab_host="TJ121"
/clone_id="Hordeum vulgare seedling green leaf EST library HVCDNA0004 (Blumeria challenged)"
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI; C.I. 16155 (M1a13) plants were greenhouse grown in the R Wise lab at Iowa State University, Ames, IA; 7 day old green seedlings were challenged with isolate A27 (AvrM1a13) of Blumeria graminis f. sp. hordei, and leaves were harvested 20 and 24 hr post-inoculation and snap frozen; uninoculated leaves were harvested 20 hr post-inoculation (Wei, Wise). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one cDNA library was made, and 1 million pfu were in vivo excised to give Bluescript SK(-) cDNA phagemids (Choi, Close). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Ming). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Ming, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Ming R, Kleinholz A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/g99pages/bgm/31/cover.html>)"

ORIGIN

Query Match 14.9%; Score 141.4; DB 2; Length 814;
Best Local Similarity 52.9%; Pred. No. 9,1e-31;
Matches 304; Conservative 0; Mismatches 271; Indels 0; Gaps 0;

60 CGTATCCCGCAGGAGTCCAGTGTGTGAAGAGTCCGGCGCTTCATCGCGCCT 119
DB CATCTTACCGGAGGAGGCTTGTATTAAGCGCTTCGCAAGTACTTCAAGACCT 252
QY 120 GACGCGCGGTTGATTTGATTTCCCTTATCGACCGCGTCCCTACCGCATTCGCT 179
DB 253 GCATCCCGGATTCACGGGCTGTCTCCCTCTGACCGCATCGCTTACGTGCACTCT 312
QY 180 GAAAGAAATCCCTTTAGACGTACCGACGCTGTGATCAACGCGCGATTAATACGAATT 239

DB 313 CAAGAGAAACCATCCCATCCCGACCACTCTGATATCAACAGATTAAGTGTCAT 372
QY 240 GACTGTGACGGCATCATATTTCAGATTAACCATCCCAATCCCTCATACGGTTC 299
DB 373 CCAATGACGGCGCTCTTACGTCAAGATTTGATTCCTACGCGTCTTATGGCGT 432
QY 300 GAGCACTCATTTATGCAATTAACCACTTGGCCCAACGACGCTGCTTATTCG 359
DB 433 GGAAGATCCCATTTTTCAGATTCATTCAGCCGACAACTATGGAAGTGGCTTGG 492
QY 360 GCGATGAGATTTGAACAAACGTTTGAAGAACGGAGAAATCAACGTAACCGTCTC 419
DB 493 AAGATTAACCTTTGACCAAGACTTTTGAAGAGAGACCATTTAGATGAAGATTGGAG 552
QY 420 CGCCCTGATGAAGACCCCGGGGCTTGAGTGAAGATCCCTCGTTACGAATCAAGA 479
DB 553 GTCCATTAATAGAGCTCGACAGACTGGGCTTGAAGTGTCTTGTACGATCAAGGA 612
QY 480 TTGGTTCGCGCGCAAGAAATCTTCCGCGCATGCGACAAATTACCGCGAACGGA 539
DB 613 CATTTCTCTCATCGGGGTGAGAAATGCTATGAGATGCAACAGAGCGAAGAGAG 672
QY 540 AAACGCGCGCGTATTTGCGCAATCCGAGGCCCTTAATGAAATCAACCTTGCAG 599
DB 673 AAACGCGCTCAAAATTTCTCCAGTCAAGGGGCTATGTGATCAGCAAAACGCGCAA 732
QY 600 TGCTACGCTGAAGCCGAATTCACCAATCCGAAG 634
DB 733 GGTGAGGCTGAACCGATTTTTCAGTCCCAAG 767

RESULT 37

LOCUS

BM459766 918 bp mRNA linear EST 05-FEB-2002
ACCESSION AGENCOURT_6417777 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5534403

VERSION 5, mRNA sequence.
KEYWORDS BM459766.1 GI:18508806

SOURCE

EST.
Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 (bases 1 to 918)
NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov

Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.llnl.gov>

Plate: LHAM12220 row: n column: 04
High quality sequence stop: 626.

FEATURES

source

1. 918
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5534403"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_71"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb."

ORIGIN

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Qy 485 TTCCCGCCGAGAAATCTTGGCGCAATGCAAGCAAAATTACCGCCGAGCCGAGAAAAC 544
Db 632 TGCCCCCTCATGAGATGCGTGTCTATGAAATCAAGCTGAAGCTGAGGTAAAGT 691
Qy 545 GCGCCCGATTTGCCGAATCCGAAGCCGTAATAATGAAACAAATGCACTTGGCAGTGTG 604
Db 692 GAGCCCAATCTTGTAGTCTGAGAGAGAAAGAAATCCCATATCAATGCTGATGTTA 751
Qy 605 AGCGTGAAGCCGAAATCCCAACATCCGAAGGCGAGGCTCAGGCTCGGTCAATGCGTCA 664
Db 752 AGAAAAGTCTGTATCTTGGATCTGAA----- 780
Qy 665 ATGCGGAGAAATTCGCCCATCAACCGCGCAAGCGGAGCGAATCCCTGCGCCTTG 724
Db 781 --GCAGAAAGATGAGACAGGATCGAGCAAGAGGAGGAGAGAACTACTAGCTA 838
Qy 725 TTGCGGAGCCCAATCCCAAGCATCCGTCAAATTTGCCCGCCCTTCAAAACCAAGCG 784
Db 839 GAGTACAAAGCTACTGCGAAAGGCGCTGTCTTGTCTTCAAGTCCCTCAAGAAACTGAGG 898
Qy 785 GGGCGGATGCGGTCAATCTGAAGATTGGCGAACAATAGTACCGCGCTTCAACAATCTTG 844
Db 899 GAGTGAAGGCGCGCGGATTTGAGATTTGAGAGCAATACATACAGCTTCCGTAACTTG 958
Qy 845 CCAAGAAAGCAATACGCTGATTTATGCCCGCAATGTTGCCGACATTCGCGAGCTGATTT 904
Db 959 CCAAGAGGATGATGATTTGTTGCTTCAAGTGTGCTTCAAAATCTCTAGCATGATTT 1018
Qy 905 CTGCGCGATGAAATTTATCGACAGC 930
Db 1019 CTCAAGCTTTAACAATGTAACAAAGC 1044

RESULT 39
CNS09PCF 924 bp mRNA linear HTC 08-JAN-2003
LOCUS Single read from an extremity of a full-length cDNA clone made from
DEFINITION Anopheles gambiae total adult females. 5-PRIME end of clone
FX0AC53BE07 of strain 6-9 of Anopheles gambiae (African malaria
mosquito).
BX068923
VERSION BX068923.1 GI:27642204
KEYWORDS
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preyoptera;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Anopheles.
1 (bases 1 to 924)
REFERENCE
AUTHORS Genoscope.
TITLE Direct Submission
JOURNALS Submitted (06-JAN-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
- web : www.genoscope.cns.fr)
Location/Qualifiers
1. 924
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="6-9"
/db_xref="taxon:7165"
/clone="FX0AC53BE07"
/plasmid="PME18S-FL"
/note="end : 5-PRIME"

FEATURES
source
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Query Match 14.7%; Score 139.6; DB 3; Length 924;
Best Local Similarity 53.9%; Pred. No. 3.3e-30;
Matches 329; Conservative 0; Mismatches 279; Indels 2; Gaps 2;

Qy 125 CCGGTTGAATATTTGATCCCTTATCGACCGGCGTCCGCTACCGCATTCGCTGAAG 184
Db 2 CCGGCTGAAGCTCTGCTGCGCGGTGTGACCGGGTGAAGTACGTGACGAGCTGAAGG 61

Qy 185 AATTCCTTTAGACGTACCCAGGCTTGATACGCGCGATATACGCAATTTGACTG 244
Db 62 AATTCGCAATGAGATGCTCCGAAACAGTCCGCACTAGCTCGACAAAGTAACTGACGA 121
Qy 245 TTGAGCGCATATCTATTTTCCAAATACCAATCCCAATCCGCTCATAGGTTGAGCA 304
Db 122 TCGAGGCTGTCTTACCTGCGCATCTCGACCCGTAACCTGCGTGTGAGTGTGAGG 181
Qy 305 ACTACATTTATGGCAATTAACCGAGCTTGCCCAAGCAAGCTGCGTTCGTTATCCGGGCTA 364
Db 182 ACCCGAGTTTGGCATCATCCAGCTCGCCAAAGAGATGCGCTCCGAGCTGGGCAAGA 241
Qy 365 TGAAGTTGACAAAACGTTTGAGAGACCGGACGAATCAAGTACCTGCTCTCCGCC 424
Db 242 TGTCACTGACAAAGTGTTCGGAGGCGCATGCTCAACATCAGCATCGTGAAGTGA 301
Qy 425 TTGATGAAGCCCGCGGCTTGGGGTGTGAAGTCTCCGTTAGAAATCAAGATTGG 484
Db 302 TC-AAAGAGCGAGCGAAGGCGGCAATCTCTGCTGCGGTACGAAATTCGCGACATCA 360
Qy 485 TTCCGCGCAAGAAATCTCTTCGCGCAATGCAAGCAAAATTAACCGCGAAGCGGAAAAC 544
Db 361 AGCTGCGAGCGCGGATGACGAGACGATGCAATGCAAGTGAAGCGGACGCGC-CAAGC 419
Qy 545 GCGCCGATTTGCCGAATCCGAAGCGCGTAATAATGAAACAATCACTTCCAGTGTG 604
Db 420 GGGCGCGATCTCGAATCGGAGGATGTCGCGCGCGCATTAACGTGGCCGAGGTTA 479
Qy 605 AGCGTGAAGCGGAATCCCAATCCGAAGCGGCTCAAGGCTGCGGTCAATGCGTCCA 664
Db 480 AGCACAAGTGGCGATCTTCTCGAGGCGCGAAGAGAGAGATCAATGCGGCGA 539
Qy 665 ATGCGGAAATATCGCCGATCAACCGCGCAAGGCGAAGCGGAATCCCTGCGCCTTG 724
Db 540 ATGCTGAAGCGCGCGCATATGCGGCGATGCGGCGATGCGGCGTGAAGTGAAGTTCG 599
Qy 725 TTGCGGAGC 734
Db 600 TGCGCGAATC 609

RESULT 40
AV434570 528 bp mRNA linear EST 23-AUG-2000
LOCUS AV434570 Porphyra yezoensis TU-1 Porphyra yezoensis cDNA clone
DEFINITION PM045a11 x 5', mRNA sequence.
AV434570
VERSION AV434570.1 GI:8589795
KEYWORDS EST.
SOURCE Porphyra yezoensis
ORGANISM Porphyra yezoensis
Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae;
Porphyra.
1 (bases 1 to 528)
REFERENCE
AUTHORS Nikaido,I., Asamizu,E., Nakajima,M., Nakamura,Y., Saga,N. and
Tabata,S.
TITLE Generation of 10,154 expressed sequence tags from a leafy
JOURNALS gematophyte of a marine red alga, Porphyra yezoensis
MEDLINE DNA Res. 7, 223-227 (2000)
PUBMED 20363100
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
1. 528
/organism="Porphyra yezoensis"
/mol_type="mRNA"
/strain="TU-1"
/db_xref="taxon:2788"
/clone="PM045a11_x"

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/note="vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"

ORIGIN

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Best Local Similarity 55.2%; Pred. No. 3.2e-30;  
Matches 272; Conservative 0; Mismatches 221; Indels 0; Gaps 0;  
  
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Db 36 TCGTCCCCAGAGAGAGATGTCAGCGCTTGTGCTTCCACCGCAAGCTGG 95  
   |||||  
QY 122 CGGCGGTTGAATTTTGAATTCCTTATGACCGCGTGCCTACCGCATTCGCTGA 181  
   |||||  
Db 96 AGCCCGGCTGAACTGATTAATCCCTGTGTGACCAAGSTCACTACATCCACTCTGA 155  
   |||||  
QY 182 AAGAAATCCCTTAAGACGTAACCGAGCTGTGATCAAGGCGATTAATAGCAATTGA 241  
   |||||  
Db 156 AGGAGAGGCGCATTCGATTCCTAATCAAGTGCCATCACCGGAGCAACGTGTCAATCA 215  
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QY 242 CTGTGACGGCATTCATCTATTTCCAAGTAACGATCCCAACTCGCTCATACGGTTTCA 301  
   |||||  
Db 216 ACCTGACGCAATTCCTGTTGCTCGGTGGAAGACCGGCTCAAGGCTGTGTAAGGAGTGG 275  
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QY 302 GCAACTACATTAATGCAATTACCCAGCTTGCCCAAGCAAGCTGCGTTCGTTATCGGCG 361  
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Db 276 AAAACCCGCGCAGGCGCATCACCTCTCGCTCAAGACGATGCGCTCCGAGCTAGGAA 335  
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QY 362 GTATGAGTTGACAAAACGTTTGAAGAACGCAAGAAATCAACAGTACCGTCTCTCGG 421  
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Db 336 AGCTCACTTGGACAAGACCTTCGAGAGAGGGAAGACCTCAACGCGGTATGTCTCGT 395  
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QY 422 CCCTGATGAAGCGCGCGGCGCTTGAGGAGTGTGAAAGTCTCTCGTTACGAATCAAGGATT 481  
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Db 396 CCATTAACGCGCGCTGCGGGGTTTGGGGCATCACTGCTGCGCTATGAAATCCGGACA 455  
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QY 482 TGGTTCCGCGCGAAGAAATCTTCCGCAATGCAAGGACAAATTAACCGCGAAACGGGAAA 541  
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Db 456 TCTCCCGCGCGCCCAACGTGCGAAGGCGATGAGGCTGCAAGCCGAACCGCGCGCA 515  
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QY 542 AACGGCGCCCGTAT 554  
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Db 516 AGCGGCTTCAGAT 528  
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OW nucleic - nucleic search, using sw model

Run on: August 13, 2005, 18:26:17 ; Search time 614 Seconds
(without alignments)
9139.926 Million cell updates/sec

Title: US-10-018-470A-16

Perfect score: 948

Sequence: 1 atgagattttcattatctt.....gcagcaaaacgcgaataaa 948

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: geneseqn19808:*
2: geneseqn19908:*
3: geneseqn20008:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	948	100.0	948	AAZ54584	Aaz54584 Neisseria
2	948	100.0	948	AAZ53752	Aaz53752 Neisseria
3	948	100.0	948	AAAB1267	AaAB1267 N. gonorr
4	948	100.0	948	AAZ51552	AaZ51552 N. gonorr
5	945	99.7	945	ABZ40185	ABZ40185 N. gonorr
6	890.4	93.9	948	AAZ53754	Aaz53754 Neisseria
7	890.4	93.9	948	AAZ54582	Aaz54582 Neisseria
8	890.4	93.9	948	AAZ54585	Aaz54585 Neisseria
9	890.4	93.9	948	AAZ53751	Aaz53751 Neisseria
10	890.4	93.9	948	AAAB1268	AaAB1268 N. mening
11	890.4	93.9	948	AAAB1265	AaAB1265 N. mening
12	890.4	93.9	948	AAZ51553	AaZ51553 N. mening
13	890.4	93.9	948	AAZ51550	AaZ51550 N. mening
14	886.6	93.5	951	AAZ54581	Aaz54581 Neisseria
15	886.6	93.5	951	AAAB1264	AaAB1264 N. gonorr
16	886.6	93.5	951	AAZ51549	AaZ51549 N. gonorr
17	877.6	92.6	948	AAZ53753	Aaz53753 Neisseria
18	877.6	92.6	948	AAZ54583	Aaz54583 Neisseria
19	877.6	92.6	948	AAAB1266	AaAB1266 N. mening
20	877.6	92.6	948	AAZ51551	AaZ51551 N. mening

21	877.6	92.6	56609	3	AAA81459	Aaa81459 N. mening
22	877.6	92.6	110000	3	AAAB1490_11	Continuation (12 o
23	877.6	92.6	349980	3	AAZ51609	AaZ51609 Neisseria
24	877.6	92.6	349980	3	AAZ51610	AaZ51610 Neisseria
25	840.4	88.6	850	3	AAZ53749	Aaz53749 Neisseria
26	547.2	57.7	600	3	AAZ54580	Aaz54580 Neisseria
27	547.2	57.7	600	3	AAAB1263	AaAB1263 N. mening
28	547.2	57.7	600	3	AAZ51548	Aaz51548 N. mening
29	544	57.4	600	3	AAZ53750	Aaz53750 Neisseria
30	174	18.4	1677	3	AAZ12730	AAZ12730 DNA encod
31	172	18.1	1296	5	AAH6657	Aah6657 C glutami
32	172	18.1	1416	10	ADD13606	Add13606 C. glutam
33	172	18.1	1419	4	AAZ71844	Aaz71844 Corynebac
34	172	18.1	1419	4	AAZ71207	Aaz71207 Corynebac
35	172	18.1	1426	10	ADD13438	Add13438 C. glutam
36	172	18.1	349980	5	AAH68529	Aah68529 C glutami
37	165.6	17.5	1153	4	ABU05449	Abu05449 Drosophil
38	160.2	16.9	1218	12	ADJ35266	Adj35266 Plant CDN
39	155.6	16.4	1071	12	ADN97415	Adn97415 Human SLP
40	155.6	16.4	1244	4	AAH13961	Aah13961 Human CDN
41	155.6	16.4	1253	12	ADQ96067	Adq96067 T cell ac
42	155.6	16.4	1273	12	ADQ87392	Adq87392 Human tum
43	155.6	16.4	1273	13	ADQ85052	Adq85052 Human tum
44	155.6	16.4	1303	13	ACN38885	Acn38885 Tumour-as
45	155.6	16.4	1303	13	ADP55143	Adp55143 Human PRO

ALIGNMENTS

RESULT 1	AAZ54584	standard; DNA; 948 BP.
ID	AAZ54584	standard; DNA; 948 BP.
AC	AAZ54584;	
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DT	15-SEP-2003	(revised)
DT	21-MAR-2000	(first entry)
XX		
DE	Neisseria gonorrhoeae ORF 519 partial DNA sequence SEQ ID NO:3053.	
XX		
KW	Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;	
KW	antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;	
KW	antibacterial; gene therapy; de.	
XX		
OS	Neisseria gonorrhoeae.	
XX		
PN	MO9957280-A2.	
XX		
PD	11-NOV-1999.	
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PF	30-APR-1999;	99WO-US009346.
XX		
PR	01-MAY-1998;	98US-0083758P.
PR	31-JUL-1998;	98US-0094869P.
PR	02-SEP-1998;	98US-0098994P.
PR	02-SEP-1998;	98US-0099062P.
PR	09-OCT-1998;	98US-0103749P.
PR	09-OCT-1998;	98US-0103794P.
PR	09-OCT-1998;	98US-0103796P.
PR	25-FEB-1999;	99US-0121528P.
XX		
PA	(CHIR) CHIRON CORP.	
PA	(GENO) INST GENOMIC RES.	
XX		
PI	Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;	
PI	Petersen J, Pizzo M, Rappuoli R, Ratti G, Scalato E, Scarbelli M;	
PI	Tetzelin H, Venter JC;	
XX		
XX		
DR	WPI; 2000-062150/05.	
XX		
XX	P-PSDB; AAY5782.	
PT	Novel Neisserial polypeptides predicted to be useful antigens for	

PT vaccines and diagnostics.
 XX Example 1; Page 76-77; 1453bp; English.
 XX
 CC AA253015 to AA254536, AA254577 to AA254615, and AAY74253 to AAY75941
 CC represent novel *Neisseria meningitidis* and *N. gonorrhoeae* polynucleotides
 CC and polypeptides. AA254537 to AA254576 and AA254616 to AA25473 represent
 CC PCR primers used in the exemplification of the present invention. The
 CC polypeptides, the polynucleotides, antibodies and compositions of the
 CC invention can be used as vaccines, as diagnostic reagents, and as
 CC immunogenic compositions. The polypeptides can be used in the manufacture
 CC of medicaments for treating or preventing infection due to *Neisseria*
 CC bacteria (e.g. meningitis and septicemia), to detect the presence of
 CC *Neisseria* bacteria, or to raise antibodies. They may also be used to
 CC screen for agonists or antagonists, which may themselves have use as
 CC antibacterial agents. The polynucleotides of the invention may also be
 CC used in gene therapy protocols. (Updated on 15-SEP-2003 to standardise OS
 CC field)

SQ Sequence 948 BP; 245 A; 278 C; 226 G; 199 T; 0 U; 0 Other;

Query Match 100.0%; Score 948; DB 3; Length 948;

Best Local Similarity 100.0%; Pred. No. 5e-276;

Matches 948; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAATTTTTCATATCTTGTGGACGCGCGCTTTCGCTTCAAAATCCTTGTG 60
 DB 1 ATGGAATTTTTCATATCTTGTGGACGCGCGCTTTCGCTTCAAAATCCTTGTG 60
 QY 61 GTATCCCCCAGAGAAAGTCCAGTGTGCGAAAGCTCGGCGCTTCATCGCGCCTG 120
 DB 61 GTATCCCCCAGAGAAAGTCCAGTGTGCGAAAGCTCGGCGCTTCATCGCGCCTG 120
 QY 121 ACGCGCGTGGTGAATTTTGAATTCCTTATCCAGCGCGCTTACCGCATTCGCTG 180
 DB 121 ACGCGCGTGGTGAATTTTGAATTCCTTATCCAGCGCGCTTACCGCATTCGCTG 180
 QY 121 ACGCGCGTGGTGAATTTTGAATTCCTTATCCAGCGCGCTTACCGCATTCGCTG 180
 DB 121 ACGCGCGTGGTGAATTTTGAATTCCTTATCCAGCGCGCTTACCGCATTCGCTG 180
 QY 181 AAAGAAATCCCTTGAAGTGAAGTCCAGCGCGCTTACCGCATTCGCTG 240
 DB 181 AAAGAAATCCCTTGAAGTGAAGTCCAGCGCGCTTACCGCATTCGCTG 240
 QY 241 ACTGTTGACGGCATCATCTTATCCAGTAAACCGATCCCAAACTGCGCTCATACGGTTG 300
 DB 241 ACTGTTGACGGCATCATCTTATCCAGTAAACCGATCCCAAACTGCGCTCATACGGTTG 300
 QY 301 AGCAACTACATTATGCAATTAACCGATTCGCGCAAGAGCTGCTTACCGCATTCGCG 360
 DB 301 AGCAACTACATTATGCAATTAACCGATTCGCGCAAGAGCTGCTTACCGCATTCGCG 360
 QY 361 CGTATGAGTGAAGCAAAAGCTTGAAGACGCGCAAGATCAACGATACCGTCTCC 420
 DB 361 CGTATGAGTGAAGCAAAAGCTTGAAGACGCGCAAGATCAACGATACCGTCTCC 420
 QY 421 GCCCTCGATGAAGCGCGCGGCTTGGGCTGGAAGTCTCCGTTACGAAATCAAGAT 480
 DB 421 GCCCTCGATGAAGCGCGCGGCTTGGGCTGGAAGTCTCCGTTACGAAATCAAGAT 480
 QY 481 TTGTTCCGCGCGCAAGAAATCCTTGGCGCAATGCGCAAAATTAACCGCAAGCGCAA 540
 DB 481 TTGTTCCGCGCGCAAGAAATCCTTGGCGCAATGCGCAAAATTAACCGCAAGCGCAA 540
 QY 541 AAACGCGCGCTATTCGCAATCCGAAGCGCTAAATTCGAACAATCAACCTTGCCAGT 600
 DB 541 AAACGCGCGCTATTCGCAATCCGAAGCGCTAAATTCGAACAATCAACCTTGCCAGT 600
 QY 601 GGTGCGGTGAAGCGCAAAATCCGAATTCGAAGCGAGCTCAGGCTCGGTCATGCG 660
 DB 601 GGTGCGGTGAAGCGCAAAATCCGAATTCGAAGCGAGCTCAGGCTCGGTCATGCG 660
 QY 661 TCCATGCGCGCAAAATGCGCGCATCAACGCGCGCAAGGCGAAGCGCAATCCTTGCGC 720
 DB 661 TCCATGCGCGCAAAATGCGCGCATCAACGCGCGCAAGGCGAAGCGCAATCCTTGCGC 720

QY 721 CTTGTTCCGGAAGCAATGCGGAAGCATCCGTCAAAATTCGCGCGCTTCAAAACCAA 780
 DB 721 CTTGTTCCGGAAGCAATGCGGAAGCATCCGTCAAAATTCGCGCGCTTCAAAACCAA 780
 QY 781 GCGCGGGCGGATGCGGTCAATCTGAACATTTGCGGAACAATGCGCGCTTCAAAACCA 840
 DB 781 GCGCGGGCGGATGCGGTCAATCTGAACATTTGCGGAACAATGCGCGCTTCAAAACCA 840
 QY 841 CTTGCGCAAAAGCAATACGCTGATTATGCGCGCAATGTTGCGCAATCGAGCGCTG 900
 DB 841 CTTGCGCAAAAGCAATACGCTGATTATGCGCGCAATGTTGCGCAATCGAGCGCTG 900
 QY 901 ATTCTGCGCGCATGAATTTATGACAGCAGCAAAAACCGCAATTA 948
 DB 901 ATTCTGCGCGCATGAATTTATGACAGCAGCAAAAACCGCAATTA 948

RESULT 2

AA253752
 ID AA253752 standard; DNA; 948 BP.

AC AA253752;

DT 15-SEP-2003 (revised)

DT 21-MAR-2003 (first entry)

DE *Neisseria gonorrhoeae* ORF 519 partial DNA sequence SEQ ID NO:1453.

KM *Neisseria meningitidis*; *Neisseria gonorrhoeae*; antigen; vaccine;

KM antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;

KM antibacterial; gene therapy; ds.

OS *Neisseria gonorrhoeae*.

PN W09957280-A2.

PD 11-NOV-1999.

PF 30-APR-1999; 99WO-US009346.

PR 01-MAY-1998; 98US-0083758P.

PR 31-JUL-1998; 98US-0094869P.

PR 02-SEP-1998; 98US-0098994P.

PR 02-SEP-1998; 98US-0099062P.

PR 09-OCT-1998; 98US-0103749P.

PR 09-OCT-1998; 98US-0103796P.

PR 09-OCT-1998; 98US-0103796P.

PR 25-FEB-1999; 99US-0121528P.

XX (CHIR -) CHIRON CORP.

PA (GENO-) INST GENOMIC RES.

PI Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M,

PI Petersen J, Pizza M, Rappuoli R, Ratti G, Scalato E, Scarselli M,

PI Tettelin H, Venter JC;

DR WPI: 2000-062150/05.

DR P-PSDB; AAY74990.

PT Novel *Neisseria* polypeptides predicted to be useful antigens for

PT vaccines and diagnostics.

PS Claim 7; Page 778-779; 1453bp; English.

CC AA253015 to AA254536, AA254577 to AA254615, and AAY74253 to AAY75941

CC represent novel *Neisseria meningitidis* and *N. gonorrhoeae* polynucleotides

CC and polypeptides. AA254537 to AA254576 and AA254616 to AA25473 represent

CC PCR primers used in the exemplification of the present invention. The

CC polypeptides, the polynucleotides, antibodies and compositions of the

CC invention can be used as vaccines, as diagnostic reagents, and as

CC immunogenic compositions. The polypeptides can be used in the manufacture

CC of medicaments for treating or preventing infection due to *Neisseria*

CC bacteria (e.g. meningitis and septicemia), to detect the presence of

CC Neisseria bacteria, or to raise antibodies. They may also be used to
 CC screen for agonists or antagonists, which may themselves have use as
 CC antibacterial agents. The polynucleotides of the invention may also be
 CC used in gene therapy protocols. (Updated on 15-SEP-2003 to standardise OS
 CC field)

XX Sequence 948 BP, 245 A, 278 C, 226 G, 199 T, 0 U, 0 Other:

Query Match 100.0%; Score 948; DB 3; Length 948;
 Best Local Similarity 100.0%; Pred. No. 5e-276;
 Matches 948; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 ATGGAATTTTTCATTATCTTGTGGCAGCCGCTTGGGCTTCAAACTCTTGTGC 60
DB 1 ATGGAATTTTTCATTATCTTGTGGCAGCCGCTTGGGCTTCAAACTCTTGTGC 60
QY 61 GTCAATCCCCCAGAGAGATCCACGCTGCGAAAGGCTGGGCGTTTCATCGCCGCTG 120
DB 61 GTCAATCCCCCAGAGAGATCCACGCTGCGAAAGGCTGGGCGTTTCATCGCCGCTG 120
QY 121 ACGGCGGTTTGAATATTTTGAATCCCTTTATCGACCGCGTCCCTACCGCATTCGCTG 180
DB 121 ACGGCGGTTTGAATATTTTGAATCCCTTTATCGACCGCGTCCCTACCGCATTCGCTG 180
QY 181 AAAAAGAAATCCCTTTAGACGTACCCAGCCAGCTGTGCATCAACGGCGATTAATACGCAATTG 240
DB 181 AAAAAGAAATCCCTTTAGACGTACCCAGCCAGCTGTGCATCAACGGCGATTAATACGCAATTG 240
QY 241 ACTGTTGAAGGAGATCATCTATTCCAGATGACGATCCCAACTGCTCATACGAGTTG 300
DB 241 ACTGTTGAAGGAGATCATCTATTCCAGATGACGATCCCAACTGCTCATACGAGTTG 300
QY 301 AGCAATCACTATATGCAATTAACCAAGCTTCCCAACGACGCTGCGTTCCGTTATCGG 360
DB 301 AGCAATCACTATATGCAATTAACCAAGCTTCCCAACGACGCTGCGTTCCGTTATCGG 360
QY 361 CGTATGAGTTGGAACAAACGTTTGAAGAACGACGAATCAACGTAACCGTCTC 420
DB 361 CGTATGAGTTGGAACAAACGTTTGAAGAACGACGAATCAACGTAACCGTCTC 420
QY 421 GCCCTCGATGAAGCCGCGCGCTTGGGGGTGAAGTCTCCGTTACGAATCAAGAT 480
DB 421 GCCCTCGATGAAGCCGCGCGCTTGGGGGTGAAGTCTCCGTTACGAATCAAGAT 480
QY 481 TTGGTTCCGCGCAAGAAATCTTCCGCGCATGACAGCAAAATTAACCGCGCAACGCGA 540
DB 481 TTGGTTCCGCGCAAGAAATCTTCCGCGCATGACAGCAAAATTAACCGCGCAACGCGA 540
QY 541 AAAACGCGCCGTTATGCGCAATCCGAAGCCGTTAAATGCAACAAATCAACTTGCAGT 600
DB 541 AAAACGCGCCGTTATGCGCAATCCGAAGCCGTTAAATGCAACAAATCAACTTGCAGT 600
QY 601 GGTGACGCTGGAAGCCGAATCCGAACATCCGAAGGCGAGGCTGAGGCTGCGTCATGCG 660
DB 601 GGTGACGCTGGAAGCCGAATCCGAACATCCGAAGGCGAGGCTGAGGCTGCGTCATGCG 660
QY 661 TCCATATGCGAAGAAATCCGCGCATCAACCGCGCAAAAGCGAGCGAATCCCTGCGC 720
DB 661 TCCATATGCGAAGAAATCCGCGCATCAACCGCGCAAAAGCGAGCGAATCCCTGCGC 720
QY 721 CTTGTTGCGAAGCCGAATCCGAAGCCATCCGTTCAATTCGCCCGCTTCAAAACCGA 780
DB 721 CTTGTTGCGAAGCCGAATCCGAAGCCATCCGTTCAATTCGCCCGCTTCAAAACCGA 780
QY 781 GGGGGGGCGGATCGGTCATCTGAAGATTGGGAAACAAATACGAGCGGTTCAACAT 840
DB 781 GGGGGGGCGGATCGGTCATCTGAAGATTGGGAAACAAATACGAGCGGTTCAACAT 840
QY 841 CTTGCCAAGAAAGCAATACGCTGATTATGCCCGCAATTTTCCGACATCGGAGCGCTG 900
DB 841 CTTGCCAAGAAAGCAATACGCTGATTATGCCCGCAATTTTCCGACATCGGAGCGCTG 900
QY 901 ATTTGCGCGCATGAAATTTATGACAGCAAGCAAAACCGCCAAATTA 948
  
```

DB 901 ATTTGCGCGCATGAAATTTATGACAGCAAGCAAAACCGCCAAATTA 948

RESULT 3
 AAA81267

ID AAA81267 standard; DNA; 948 BP.

XX AAA81267;

XX 15-SEP-2003 (revised)
 DT 04-DEC-2000 (first entry)

XX N. gonorrhoeae partial DNA sequence g519-1.seq SEQ ID NO:976.

XX Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;
 KW antigen; vaccine; diagnosis; infection; antibacterial; identification;
 KW Meningococcus B; MemB; ds.

XX Neisseria gonorrhoeae.

XX WO200022430-A2.

XX 20-APR-2000.

XX 08-OCT-1999; 99WO-US023573.

XX 09-OCT-1998; 98US-0103794P.

XX 30-APR-1999; 99US-0132068P.

XX (CHIR) CHIRON CORP.

XX Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC,
 PI Massignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V,
 PI Rappelli R, Pizzi M;

XX WPI: 2000-318079/27.

XX P-PSDB; AAB25627.

XX Isolated nucleotide sequences of Neisseria meningitidis which can be used
 PT in the diagnosis and treatment of N. meningitidis infection and other
 PT Neisserial infections, for example, N.gonorrhoea.

XX Claim 9; Page 73-74; 1760bp; English.

XX The present invention describes methods of obtaining immunogenic proteins
 CC from Neisseria genomic sequences. AAA81453 to AAA82414 represent
 CC specifically claimed Neisseria meningitidis genomic DNA sequences;
 CC AAA81260 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DNA
 CC sequences and their corresponding proteins; AAA81254 to AAA81259 and
 CC AAA81304 to AAA81321 represent PCR primers used in the isolation of
 CC Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent
 CC Neisseria meningitidis MemB polynucleotide ORF sequences, which are all
 CC used in the exemplification of the present invention. The nucleic acid
 CC sequences, protein sequences, and antibodies against them, can be used in
 CC the manufacture of a composition. The composition can be used as a
 CC medicament (or in the manufacture of a medicament) for treating,
 CC preventing or diagnosing infection due to Neisserial bacteria. For
 CC example, some of the identified proteins could be components of vaccines
 CC against Meningococcus B; against all serotypes; and/or against all
 CC pathogenic Neisseriae. Identification of sequences from the bacterium
 CC will also facilitate production of biological probes, particularly
 CC organism-specific probes. Attempts to make efficacious Meningococcus B
 CC vaccines have also been tried but none have successfully overcome
 CC antigenic variability. The provision of further, complete sequences may
 CC provide an opportunity to identify secreted or surface exposed proteins
 CC that may be presumed targets for the immune system and which are not
 CC antigenically variable or at least more conserved than other more
 CC variable regions. (Updated on 15-SEP-2003 to standardise OS field)

XX Sequence 948 BP, 245 A, 278 C, 226 G, 199 T, 0 U, 0 Other;

Query Match 100.0%; Score 948; DB 3; Length 948;
 Best Local Similarity 100.0%; Pred. No. 5e-276;
 Matches 948; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAATTTTCATTATCTTGTGGACGCGCTGCGCTTTGGCTTGAATCCTTTGTC 60
 DB 1 ATGGAATTTTCATTATCTTGTGGACGCGCTGCGCTTTGGCTTGAATCCTTTGTC 60
 QY 61 GTTCATCCCCCAGAGAGAGTCCAGCTGTGCGAAAGAGCTCGGGCGTTTCATCGGCGCTG 120
 DB 61 GTTCATCCCCCAGAGAGAGTCCAGCTGTGCGAAAGAGCTCGGGCGTTTCATCGGCGCTG 120
 QY 121 ACGGCGGTTTGAATATTTTGAATTCCTTATCGACCGGCTGCGCTTACCGCATTCGCTG 180
 DB 121 ACGGCGGTTTGAATATTTTGAATTCCTTATCGACCGGCTGCGCTTACCGCATTCGCTG 180
 QY 181 AAAGAAATCCCTTTAGAGTACCCAGCGAGTCTGTCATCAGCGGATTAATACGCAATTTG 240
 DB 181 AAAGAAATCCCTTTAGAGTACCCAGCGAGTCTGTCATCAGCGGATTAATACGCAATTTG 240
 QY 241 ACTGTTGACGGCATCTATTTTCAAGTAAACCGATCCCAATCTGCGCTCATAGCGTTTCG 300
 DB 241 ACTGTTGACGGCATCTATTTTCAAGTAAACCGATCCCAATCTGCGCTCATAGCGTTTCG 300
 QY 301 AGCAACTACATTTATGCAATTTACCGAGCTTGGCCCAAGACGCTGCTTCCGTTATCGG 360
 DB 301 AGCAACTACATTTATGCAATTTACCGAGCTTGGCCCAAGACGCTGCTTCCGTTATCGG 360
 QY 361 CGTATGAGTTTGACAAACGTTTGAAGACGCGACGAATTAACAATACGTCGCTCTCC 420
 DB 361 CGTATGAGTTTGACAAACGTTTGAAGACGCGACGAATTAACAATACGTCGCTCTCC 420
 QY 421 GCGCTCGATGAAGCGCGCGGGGCTTGGGGTGTGAAGTCTCGTTACGAATCAAGAT 480
 DB 421 GCGCTCGATGAAGCGCGGGGCTTGGGGTGTGAAGTCTCGTTACGAATCAAGAT 480
 QY 481 TTGTTTCCGCGCAAGAAATCCTTGGCGCATGACGACCAATTAACGCGCAACGCGAA 540
 DB 481 TTGTTTCCGCGCAAGAAATCCTTGGCGCATGACGACCAATTAACGCGCAACGCGAA 540
 QY 541 AAAGCGCGCGTATTTGCGCAATCCGAGCGCTTAATTAATGAAACAATCAACTTTCGCA 600
 DB 541 AAAGCGCGCGTATTTGCGCAATCCGAGCGCTTAATTAATGAAACAATCAACTTTCGCA 600
 QY 601 GGTTCAGCGTGAAGCGCGAAATCCCAACATCCGAAGGCGAGCTCAGGCTCGGCTCAATG 660
 DB 601 GGTTCAGCGTGAAGCGCGAAATCCCAACATCCGAAGGCGAGCTCAGGCTCGGCTCAATG 660
 QY 661 TTCAAATGCGAGAAATCGCCCGCATCAACCGCGCCAAAGGCGAAAGCGGAATCCTTGC 720
 DB 661 TTCAAATGCGAGAAATCGCCCGCATCAACCGCGCCAAAGGCGGAATCCTTGC 720
 QY 721 CTTGTTGCGCAAGCCCAATGCGCAAGCCATCCGTCAAATTTGGCGCGCTTAAACCCAA 780
 DB 721 CTTGTTGCGCAAGCCCAATGCGCAAGCCATCCGTCAAATTTGGCGCGCTTAAACCCAA 780
 QY 781 GCGCGGCGGAGTCCGCTCAATCTGAAGATTTGGGAAACAATATGATGCGCGCTTCAACAT 840
 DB 781 GCGCGGCGGAGTCCGCTCAATCTGAAGATTTGGGAAACAATATGATGCGCGCTTCAACAT 840
 QY 841 CTTGCGCAAGAAAGAAATACGCTGATTTATGCGCGCAATGTTGCCGACATCGGCGCTG 900
 DB 841 CTTGCGCAAGAAAGAAATACGCTGATTTATGCGCGCAATGTTGCCGACATCGGCGCTG 900
 QY 901 ATTTCGCGCGATGAATAATTAATGACGACGACGAAACCGCGCAATTA 948
 DB 901 ATTTCGCGCGATGAATAATTAATGACGACGACGCAAAACCGCGCAATTA 948

RESULT 4
 AAF21552
 ID AAF21552 standard; DNA; 948 BP.
 XX

AC AAF21552;
 XX 15-SEP-2003 (revised)
 DT 13-MAR-2001 (first entry)
 DE N. gonorrhoeae partial DNA sequence g519-1.seq SEQ ID NO:16.
 KW Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;
 KW diagnosis; antigen; detection; infection; gene therapy; antibacterial;
 KW ds.
 OS Neisseria gonorrhoeae.
 PN WO20006791-A1.
 PD 09-NOV-2000.
 PF 08-MAR-2000; 2000WO-US005928.
 PR 30-APR-1999; 99US-0132068P.
 PR 08-OCT-1999; 99WO-US023573.
 PR 28-FEB-2000; 2000GB-00004695.
 XX (CHIR) CHIRON CORP.
 PA (GENO-) INST GENOMIC RES.
 XX
 PI Pizza M, Hickey E, Peterson J, Tettelin H, Venter JC;
 PI Maignani V, Galeotti C, Mora M, Ratti G, Scariselli M, Scarlato V;
 PI Rappuoli R, Frazer CM, Grandi G;
 DR WPI; 2000-647603/62.
 DR P-PSDB; AAB58557.
 XX
 PT Neisseria meningitidis B full length genome sequence and open reading
 PT frames are used to detect, treat and prevent Neisserial infections.
 XX
 PS Example 1; Page 74; 692dp; English.
 XX
 CC The present invention describes the full length genome of Neisseria
 CC meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613
 CC represent fragments of the NMB genomic sequence, as the sequence was too
 CC long to go in a record on its own it was split into 8 sequences which
 CC overlap each other at the beginning and end of each sequence by 49980 bp
 CC (i.e. the last 49980 bp of AAF21544 is repeated at the beginning of
 CC AAF21607, the last 49980 bp of AAF21607 are repeated at the beginning of
 CC AAF21608, and so on). AAF21545 to AAF21588 encode the Neisseria proteins
 CC given in AAB58550 to AAB58593, and AAF21589 to AAF21606 represent PCR
 CC primers which are used in the exemplification of the present invention.
 CC The NMB genome and fragments from it have antibacterial activity, and can
 CC be used in vaccines and gene therapy. Neisseria nucleic acids, proteins
 CC and/or antibodies which binds to the proteins can be used in compositions
 CC for treating or preventing infection due to Neisserial bacteria or as a
 CC diagnostic reagent for detecting the presence of Neisserial bacteria or
 CC of antibodies raised to Neisserial bacteria. Computers, computer memory,
 CC computer storage medium or computer databases can be used in a search to
 CC identify open reading frames (ORFs) or coding sequences within the NMB
 CC genome. The DNA sequences provide further opportunities to find antigenic
 CC or immunogenic proteins which are more effective in vaccines than the
 CC outer membrane proteins currently used. (Updated on 15-SEP-2003 to
 CC standardise OS field)
 XX
 SQ Sequence 948 BP; 245 A; 278 C; 226 G; 199 T; 0 U; 0 Other;

Query Match 100.0%; Score 948; DB 3; Length 948;
 Best Local Similarity 100.0%; Pred. No. 5e-276;
 Matches 948; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAATTTTCATTATCTTGTGGACGCGCTGCGCTTTGGCTTGAATCCTTTGTC 60
 DB 1 ATGGAATTTTCATTATCTTGTGGACGCGCTGCGCTTTGGCTTGAATCCTTTGTC 60
 QY 61 GTTCATCCCCCAGAGAGAGTCCAGCTGTGCGAAAGAGCTCGGGCGTTTCATCGGCGCTG 120
 DB 61 GTTCATCCCCCAGAGAGAGTCCAGCTGTGCGAAAGAGCTCGGGCGTTTCATCGGCGCTG 120

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Db      61  GTGATCCCCGACGAAAGTCCAGTGTGCGAAAGGCTCGGGCGTTTCATCGGCCCTG 120
Oy      121  ACGGCGGTTTGAATATTTTGAATCCCTTATGACCGCGGTGCTTACCGCATTCGCTG 180
Db      121  ACGGCGGTTTGAATATTTTGAATCCCTTATGACCGCGGTGCTTACCGCATTCGCTG 180
Oy      181  AAGAAATCCCTTGAAGTACCGACCGCGGTGCTTATGACCGCGGTGCTTATGACCG 240
Db      181  AAGAAATCCCTTGAAGTACCGACCGCGGTGCTTATGACCGCGGTGCTTATGACCG 240
Oy      241  ACTGTGACGCGCATCTATTTCAGTAACGATCCCAATCTGCGCTCATACGCTTGC 300
Db      241  ACTGTGACGCGCATCTATTTCAGTAACGATCCCAATCTGCGCTCATACGCTTGC 300
Oy      301  AGCAATCATATTATGCAATTAACCAAGCTTGCCTTGCCTTGCCTTATCGGG 360
Db      301  AGCAATCATATTATGCAATTAACCAAGCTTGCCTTGCCTTGCCTTATCGGG 360
Oy      361  CGTATGAGTGTGACAAACGTTTGAAGAACCGGACGAAATCAACAGTACCGTCTCC 420
Db      361  CGTATGAGTGTGACAAACGTTTGAAGAACCGGACGAAATCAACAGTACCGTCTCC 420
Oy      421  GGCCTGATGAAAGCGCGCGGGCTTGGGGTGTGAAGTCTCCGTTACGAAATCAAGAT 480
Db      421  GGCCTGATGAAAGCGCGCGGGCTTGGGGTGTGAAGTCTCCGTTACGAAATCAAGAT 480
Oy      481  TTGGTTCGCGCGCAAGAAATCCTTGCAGATGCAAGCAAAATTAACCGCGAAACCGGA 540
Db      481  TTGGTTCGCGCGCAAGAAATCCTTGCAGATGCAAGCAAAATTAACCGCGAAACCGGA 540
Oy      541  AAACGCGCGCTTATTCGCGAATCCGAAGCCGTTAAATGAAATCAATCAACTTGCAGT 600
Db      541  AAACGCGCGCTTATTCGCGAATCCGAAGCCGTTAAATGAAATCAATCAACTTGCAGT 600
Oy      601  GGTGACGCGTGAAGCCGAAATCCGAATCCGAAGCCGTTAAATGAAATCAATCAACTTGCAGT 660
Db      601  GGTGACGCGTGAAGCCGAAATCCGAATCCGAAGCCGTTAAATGAAATCAATCAACTTGCAGT 660
Oy      661  TCCAAATGCGGAAATTCGCGCGCATCAACCGCGCGAAAGCGGAAATCCCTGCGC 720
Db      661  TCCAAATGCGGAAATTCGCGCGCATCAACCGCGCGAAAGCGGAAATCCCTGCGC 720
Oy      721  CTTGTTGCGGAAAGCGCATATCCGATCCGTAATTCGCGCGCTTCAAAATCCAA 780
Db      721  CTTGTTGCGGAAAGCGCATATCCGATCCGTAATTCGCGCGCTTCAAAATCCAA 780
Oy      781  GCGCGGCGGATGCGGTCATCTGAAGTTGCGGAAATCAATGAGCGGCTTCAAT 840
Db      781  GCGCGGCGGATGCGGTCATCTGAAGTTGCGGAAATCAATGAGCGGCTTCAAT 840
Oy      841  CTTGCGAAAGAAAGCAATACGCTGATTAATGCGCGCAATGTTGCGGCAATCGGCAAGCTG 900
Db      841  CTTGCGAAAGAAAGCAATACGCTGATTAATGCGCGCAATGTTGCGGCAATCGGCAAGCTG 900
Oy      901  ATTTCGCGGATGAAATTTATGACAGACGCAAAACCGCCAAATTA 948
Db      901  ATTTCGCGGATGAAATTTATGACAGACGCAAAACCGCCAAATTA 948

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RESULT 5
ABZ40185
ID ABZ40185 standard; DNA; 945 BP.

XX ABZ40185;

XX 07-MAR-2003 (first entry)

XX N. gonorrhoeae nucleotide sequence SEQ ID 4959.

XX Antibacterial; infection; vaccine; gene therapy; gene; ds.

OS Neisseria gonorrhoeae.

XX

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PN      W0200279243-AZ.
XX      10-OCT-2002.
XX      12-FEB-2002; 2002WO-IB002069.
XX      12-FEB-2001; 2001GB-00003424.
XX      (CHIR-) CHIRON SPA.
XX      Fontana MR, Pizza M, Masignani V, Monaci E,
XX      WPI: 2003-058415/05.
XX      P-PSDB; ABP79215.
XX      New protein from Neisseria gonorrhoeae, useful for the manufacture of a
XX      medicament for treating or preventing N. gonorrhoeae infection.
XX      Disclosure; Page 551; 815pp; English.
XX      The present invention relates to proteins from Neisseria gonorrhoeae.
XX      CC Also disclosed are the nucleic acid molecules encoding the proteins and
XX      CC antibodies that specifically bind to the proteins. The composition
XX      CC comprising the protein, nucleic acid or antibody is useful for the
XX      CC manufacture of a medicament for treating or preventing N. gonorrhoeae
XX      CC infection, this may be in the form of a vaccine or gene therapy.
XX      CC Sequences given in records ABZ37706-ABZ42016 represent nucleic acid
XX      CC molecules of the invention
SQ      Sequence 945 BP; 243 A; 278 C; 226 G; 198 T; 0 U; 0 Other;

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Query Match 99.7%; Score 945; DB 10; Length 945;

Best Local Similarity 100.0%; Pred. No. 4e-275;

Matches 945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy      1  ATGGAATTTTCAATATCTTGTGGACGCGTTCGCTTTCGCTTCAATCCTTTGTC 60
Db      1  ATGGAATTTTCAATATCTTGTGGACGCGTTCGCTTTCGCTTCAATCCTTTGTC 60
Oy      61  GTGATCCCCGACGAAAGTCCAGTGTGCGAAAGGCTCGGGCTTTCATGCGGCCCTG 120
Db      61  GTGATCCCCGACGAAAGTCCAGTGTGCGAAAGGCTCGGGCTTTCATGCGGCCCTG 120
Oy      121  ACGGCGGTTTGAATATTTTGAATCCCTTATGACCGCGGTGCTTACCGCATTCGCTG 180
Db      121  ACGGCGGTTTGAATATTTTGAATCCCTTATGACCGCGGTGCTTACCGCATTCGCTG 180
Oy      181  AAGAAATCCCTTGAAGTACCGACCGCGGTGCTTATGACCGCGGTGCTTATGACCG 240
Db      181  AAGAAATCCCTTGAAGTACCGACCGCGGTGCTTATGACCGCGGTGCTTATGACCG 240
Oy      241  ACTGTGACGCGCATCTATTTCAGTAACGATCCCAATCTGCGCTCATACGCTTGC 300
Db      241  ACTGTGACGCGCATCTATTTCAGTAACGATCCCAATCTGCGCTCATACGCTTGC 300
Oy      301  AGCAATCATATTATGCAATTAACCAAGCTTGCCTTGCCTTATCGGG 360
Db      301  AGCAATCATATTATGCAATTAACCAAGCTTGCCTTGCCTTATCGGG 360
Oy      361  CGTATGAGTGTGACAAACGTTTGAAGAACCGGACGAAATCAACAGTACCGTCTCC 420
Db      361  CGTATGAGTGTGACAAACGTTTGAAGAACCGGACGAAATCAACAGTACCGTCTCC 420
Oy      421  GGCCTGATGAAAGCGCGCGGGCTTGGGGTGTGAAGTCTCCGTTACGAAATCAAGAT 480
Db      421  GGCCTGATGAAAGCGCGCGGGCTTGGGGTGTGAAGTCTCCGTTACGAAATCAAGAT 480
Oy      481  TTGGTTCGCGCGCAAGAAATCCTTGCAGATGCAAGCAAAATTAACCGCGAAACCGGA 540
Db      481  TTGGTTCGCGCGCAAGAAATCCTTGCAGATGCAAGCAAAATTAACCGCGAAACCGGA 540
Oy      541  AAACGCGCGCTTATTCGCGAATCCGAAGCCGTTAAATGAAATCAATCAACTTGCAGT 600

```

Db 541 AAACGCGCCGATTTATGCGCATTCGAAAGCCGTTAAATCGAACCAATCACTTGCAGT 600
Qy 601 GGTGACGCGTGAAGCCGGAATTCGAACATTCGAAAGCGAGGCTCAGGCTGCGGTCAATGCG 660
Db 601 GGTGACGCGTGAAGCCGGAATTCGAACATTCGAAAGCGAGGCTCAGGCTGCGGTCAATGCG 660
Qy 661 TCCAAATGCGGAAATTCGCGCCGATCAACCGCGCCAAAGGCGAAGCGGAATCCCTGCGC 720
Db 661 TCCAAATGCGGAAATTCGCGCCGATCAACCGCGCCAAAGGCGAAGCGGAATCCCTGCGC 720
Qy 721 CTGTTGCGGAAAGCCGATTCGCAAGCCATTCGCAATTCGCGCCGCTTCAAAACCA 780
Db 721 CTGTTGCGGAAAGCCGATTCGCAAGCCATTCGCAATTCGCGCCGCTTCAAAACCA 780
Qy 781 GCGCGGCGGATGCGGTCAATCTGAAGATTGCGGAACATATAGTCCGCGTTCAACAT 840
Db 781 GCGCGGCGGATGCGGTCAATCTGAAGATTGCGGAACATATAGTCCGCGTTCAACAT 840
Qy 841 CTGTCGCAAGAAAGCAATACGCTGATTTATGCGCCGCAATGTTGCCGACATCGGACCTG 900
Db 841 CTGTCGCAAGAAAGCAATACGCTGATTTATGCGCCGCAATGTTGCCGACATCGGACCTG 900
Qy 901 ATTTCGCGGATGAAATTTATCGACAGCAGCAAAACCGCCAA 945
Db 901 ATTTCGCGGATGAAATTTATCGACAGCAGCAAAACCGCCAA 945

RESULT 6

AA253754
ID AA253754 standard; DNA; 948 BP.

AC AA253754;

DT 21-MAR-2000 (first entry)

DE Neisseria meningitidis ORF 519 partial DNA sequence SNU ID NO:1457.

KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;

KW antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;

KW antibacterial; gene therapy; ds.

OS Neisseria meningitidis.

PN WO957280-A2.

PD 11-NOV-1999.

PF 30-APR-1999; 99WO-US009346.

PR 01-MAY-1998; 98US-0083758P.

PR 31-JUL-1998; 98US-0094869P.

PR 02-SEP-1998; 98US-0098994P.

PR 02-SEP-1998; 98US-0099062P.

PR 09-OCT-1998; 98US-0103749P.

PR 09-OCT-1998; 98US-0103794P.

PR 09-OCT-1998; 98US-0103796P.

PR 25-FEB-1999; 99US-0121528P.

PA (CHIR) CHIRON CORP.

PA (GENO-) INST GENOMIC RES.

PI Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;

PI Petersen J, Pizzo M, Rappoli R, Ratti G, Scalato E, Scarselli M;

PI Tettelin H, Venter JC;

XX WPI; 2000-062150/05.

XX P-PSDB; AAY74992.

XX Novel Neisserial polypeptides predicted to be useful antigens for

XX vaccines and diagnostics.

XX Claim 7, Page 780; 1453pp; English.

CC AA253015 to AA254536, AA254577 to AA254615, and AAY74253 to AAY75941
CC represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides
CC and polypeptides. AA254537 to AA254576 and AA254616 to AA254673 represent
CC PCR primers used in the exemplification of the present invention. The
CC polypeptides, the polynucleotides, antibodies and compositions of the
CC invention can be used as vaccines, as diagnostic reagents, and as
CC immunogenic compositions. The polypeptides can be used in the manufacture
CC of medicaments for treating or preventing infection due to Neisserial
CC bacteria (e.g. meningitis and septicaemia), to detect the presence of
CC Neisseria bacteria, or to raise antibodies. They may also be used to
CC screen for agonists or antagonists, which may themselves have use as
CC antibacterial agents. The polynucleotides of the invention may also be
CC used in gene therapy protocols

XX Sequence 948 BP; 244 A; 270 C; 227 G; 207 T; 0 U; 0 Other;

Query Match 93.9%; Score 890.4; DB 3; Length 948;

Best Local Similarity 96.2%; Pred. No. 1.3e-258;

Matches 912; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 1 AAGGAATTTTCATTTATCTGTGCGAGCCGTCGCGCTTTCGCTTCAATCTTGTG 60
Db 1 AAGGAATTTTCATTTATCTGTGCGAGCCGTCGCTTTCGCTTCAATCTTGTG 60
Qy 61 GTCAATCCCCAGAGAAAGTCACGTTGTCGAAAGGCTCGGCGCTTTCATCGCGCCTG 120
Db 61 GTCAATCCCCAGAGAAAGTCACGTTGTCGAAAGGCTCGGCGCTTTCATCGCGCCTG 120
Qy 121 ACGGCGGTTTGAAATTTTATTTGATTCCTTTATCGACCGCGCTGCTTACCGGCAATTCG 180
Db 121 ACGGCGGTTTGAAATTTTATTTGATTCCTTTATCGACCGCGCTGCTTACCGGCAATTCG 180
Qy 181 AAGGAATCCCTTTAGACGTACCCAGCCAGGCTGTCATCAAGCGATATATACCAATTTG 240
Db 181 AAGGAATCCCTTTAGACGTACCCAGCCAGGCTGTCATCAAGCGATATATACCAATTTG 240
Qy 241 ACTGTTGACGCGATCATTTATTTCAAGTAACGATCCCAACTGCGCTCATACGCTTTCG 300
Db 241 ACTGTTGACGCGATCATTTATTTCAAGTAACGATCCCAACTGCGCTCATACGCTTTCG 300
Qy 301 AGCAACTCATTTATGCGCAATTAACCAAGTTGCCCAAGAGCGTTCGCTTATTCGCG 360
Db 301 AGCAACTCATTTATGCGCAATTAACCAAGTTGCCCAAGAGCGTTCGCTTATTCGCG 360
Qy 361 CGTATGAGTTGGAACAACGTTTGAAGAGCGGACGCAAAATCAACAAGTACGCTGCTCC 420
Db 361 CGTATGAGTTGGAACAACGTTTGAAGAGCGGACGCAAAATCAACAAGTACGCTGCTCC 420
Qy 421 GCCCTCGATGAAGCCGCGCGGCTTGGGCTGTAAGAGTCTTCGTTACGAATCAAGAT 480
Db 421 GCCCTCGATGAAGCCGCGCGGCTTGGGCTGTAAGAGTCTTCGTTACGAATCAAGAT 480
Qy 481 TTGTTGCGCGGCAAGAAATCCTTCGCGCAATGCAAGGCAAAATTAACCGCGGAACG 540
Db 481 TTGTTGCGCGGCAAGAAATCCTTCGCGCAATGCAAGGCAAAATTAACCGCGGAACG 540
Qy 541 AAACGCGCGGATTTGCGGATTCGGAAGCGCGTAAATTCGAACAATCAACTTGCAGT 600
Db 541 AAACGCGCGGATTTGCGGATTCGGAAGCGCGTAAATTCGAACAATCAACTTGCAGT 600
Qy 601 GGTGACGCGTGAAGCCGGAATTCGAACATTCGAAAGCGAGGCTCAGGCTGCGGTCAATGCG 660
Db 601 GGTGACGCGTGAAGCCGGAATTCGAACATTCGAAAGCGAGGCTCAGGCTGCGGTCAATGCG 660
Qy 661 TCCAAATGCGGAAATTCGCGCCGATCAACCGCGCCAAAGGCGAAGGCGGAATCCCTGCGC 720
Db 661 TCCAAATGCGGAAATTCGCGCCGATCAACCGCGCCAAAGGCGAAGGCGGAATCCCTGCGC 720
Qy 721 CTGTTGCGGAAAGCCGATTCGCAAGCCATTCGCAATTCGCGCCGCTTCAAAACCA 780
Db 721 CTGTTGCGGAAAGCCGATTCGCAAGCCATTCGCAATTCGCGCCGCTTCAAAACCA 780
Qy 781 GCGCGGCGGATGCGGTCAATCTGAAGATTGCGGAACATATAGTCCGCGTTCAACAT 840

XX AA254585;
AC 21-MAR-2000 (first entry)
XX
DT
XX
DE Neisseria meningitidis ORF 519 partial DNA sequence SEQ ID NO:3055.
XX
XX Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
KM antibacterial; gene therapy; ds.
XX
XX Neisseria meningitidis.
OS
XX
XX MO957280-A2.
PN
XX
PD 11-NOV-1999.
XX
PF 30-APR-1999; 99WO-US009346.
XX
PR 01-MAY-1998; 98US-0083758P.
XX
PR 31-JUN-1998; 98US-0094869P.
XX
PR 02-SEP-1998; 98US-0098999P.
XX
PR 02-SEP-1998; 98US-0099062P.
XX
PR 09-OCT-1998; 98US-0103749P.
XX
PR 09-OCT-1998; 98US-0103794P.
XX
PR 25-FEB-1999; 99US-0121528P.
XX
PA (CHIR) CHIRON CORP.
XX
PA (GENO-) INST GENOMIC RES.
XX
XX Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;
PI Peterson J, Pizzi M, Rapuoli R, Ratti G, Scalato E, Scarselli M;
PI Tettelin H, Venter JC;
XX
XX WPI; 2000-062150/05.
DR P-PSDB; AAY75783.
XX
XX Novel Neisserial polypeptides predicted to be useful antigens for
PT vaccines and diagnostics.
XX
XX Example 1; Page 77-78; 1453p; English.
PS
XX AA253015 to AA254536, AA254577 to AA254615, and AAY74253 to AAY75941
XX represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides
XX and polypeptides. AA254537 to AA254576 and AA254616 to AA255473 represent
XX PCR primers used in the exemplification of the present invention. The
XX polypeptides, the polynucleotides, antibodies and compositions of the
XX invention can be used as vaccines, as diagnostic reagents, and as
XX immunogenic compositions. The polypeptides can be used in the manufacture
XX of medicaments for treating or preventing infection due to Neisserial
XX bacteria (e.g. meningitis and septicemia), to detect the presence of
XX Neisseria bacteria, or to raise antibodies. They may also be used to
XX screen for agonists or antagonists, which may themselves have use as
XX antibacterial agents. The polynucleotides of the invention may also be
XX used in gene therapy protocols
XX
XX Sequence 948 BP; 244 A; 270 C; 227 G; 207 T; 0 U; 0 Other;
SQ
Query Match 93.9%; Score 890.4; DB 3; Length 948;
Best Local Similarity 96.2%; Pred. No. 1.3e-258;
Matches 912; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

DB 121 ACGCGCGTTGTAATATTTGATTCCTTTATCGACCGCGCTACCGCATTCGCTG 180
QY 181 AAAGAAATCCCTTTAGACGTACCCAGCGAGGTGTGCATCAAGCGGATTAATACCAATTTG 240
DB 181 AAAGAAATCCCTTTAGACGTACCCAGCGAGGTGTGCATCAAGCGGATTAATACCAATTTG 240
QY 241 ACTGTTGACGGCATCATCTATTTTCCAAAGTACCGATCCAAATCGCCTCATACGTTTGG 300
DB 241 ACTGTTGACGGCATCATCTATTTTCCAAAGTACCGATCCAAATCGCCTCATACGTTTGG 300
QY 301 AGCAACTCATATTATGAGCAATTAACCCAGCTTCCCAAGAGAGCTGCTCCGTTATCGGG 360
DB 301 AGCAACTCATATTATGAGCAATTAACCCAGCTTCCCAAGAGAGCTGCTCCGTTATCGGG 360
QY 361 CGTATGAGATTGACAAAGCGTTTGAAGAGACGCGAATATCAACAGTACCGTCTCC 420
DB 361 CGTATGAGATTGACAAAGCGTTTGAAGAGACGCGAATATCAACAGTACCGTCTCC 420
QY 421 GCCCTCGATGAAAGCGCGCGGCTTGGGAGTGTGAAGTCTCCGTTACGAATCAAGAT 480
DB 421 GCCCTCGATGAAAGCGCGCGGCTTGGGAGTGTGAAGTCTCCGTTACGAATCAAGAT 480
QY 481 TTGTTCCGCGCGAAGAAATCTTTCGCGCAATGCAAGCAAAATTAACCGCGAAGCGGAA 540
DB 481 TTGTTCCGCGCGAAGAAATCTTTCGCGCAATGCAAGCGGCAAAATTAACCGCGAAGCGGAA 540
QY 541 AAACGCGCGGATATGCGCAATTCGGAAGCGGCTAAATTCGAACAAATCAACTTCGCGAGT 600
DB 541 AAACGCGCGGATATGCGCAATTCGGAAGCGGCTAAATTCGAACAAATCAACTTCGCGAGT 600
QY 601 GGTGAGCGTGAAGCGCAATTCGAACAAATTCGGAAGCGGCTCAAGCTGCGGTCAATTCG 660
DB 601 GGTGAGCGCGAAGCGCAATTCGAACAAATTCGGAAGCGGCTCAAGCTGCGGTCAATTCG 660
QY 661 TCCAATGCCGGAAGAAATGCGCGCATCAACCGCGCAAGCGGAAATTCCTGCGC 720
DB 661 TCCAATGCCGGAAGAAATGCGCGCATCAACCGCGCAAGCGGAAATTCCTGCGC 720
QY 721 CTTGTTGCCGAAGCAATTCGGAAGCGGCTCAATTCGGAAGCGGCTCAATTCGGAAGCGGCT 780
DB 721 CTTGTTGCCGAAGCAATTCGGAAGCGGCTCAATTCGGAAGCGGCTCAATTCGGAAGCGGCT 780
QY 781 GCGCGGCGGATGCGGTCAATTCGAAGATTGCGGAACCAATTCGAGCGGCTTCAACAT 840
DB 781 GCGCGGCGGATGCGGTCAATTCGAAGATTGCGGAACCAATTCGAGCGGCTTCAACAT 840
QY 841 CTTGCGCAAGAAAGCAATTCGCTATTAATGCGCGCAATGTTGCGCAATGCGAGCGCTG 900
DB 841 CTTGCGCAAGAAAGCAATTCGCTATTAATGCGCGCAATGTTGCGCAATGCGAGCGCTG 900
QY 901 ATTCTGCGGATGAATAATTAATGAGCAAGCAAGAAACCGCAATTA 948
DB 901 ATTCTGCGGATGAATAATTAATGAGCAAGCAAGAAACCGCAATTA 948
RESULT 9
AA253751
ID AA253751 standard; DNA; 948 BP.
XX
XX AA253751;
AC 21-MAR-2000 (first entry)
XX
XX
XX Neisseria meningitidis ORF 519 partial DNA sequence SEQ ID NO:1451.
XX
XX
XX Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
KM antibacterial; gene therapy; ds.
XX
XX Neisseria meningitidis.
OS
XX
XX MO957280-A2.
XX
XX

PD 11-NOV-1999.
 XX 30-APR-1999; 99WO-US009346.
 XX 01-MAY-1998; 98US-0083758P.
 PR 31-JUL-1998; 98US-0094869P.
 PR 02-SEP-1998; 98US-0098994P.
 PR 02-SEP-1998; 98US-0099062P.
 PR 09-OCT-1998; 98US-0103749P.
 PR 09-OCT-1998; 98US-0103794P.
 PR 09-OCT-1998; 98US-0103796P.
 PR 25-FEB-1999; 99US-0121528P.
 XX (CHIR) CHIRON CORP.
 PA (GENO-) INST GENOMIC RES.
 XX Frazer C, Galeotti C, Grandi G, Hickey E, Maignani V, Mora M,
 PI Petersen J, Pizsa M, Rappuoli R, Ratti G, Scalato E, Scarselli M,
 PI Tettelin H, Venter JC;
 DR WPI: 2000-062150/05.
 XX P-PSDB; AAY74989.
 XX Novel *Neisserial* polypeptides predicted to be useful antigens for
 PT vaccines and diagnostics.
 PS Claim 7; Page 777-778; 1453pp; English.
 CC AA254015 to AA254536, AA254577 to AA254615, and AAY74253 to AAY75941
 CC represent novel *Neisseria meningitidis* and *N. gonorrhoeae* polynucleotides
 CC and polypeptides. AA254537 to AA254576 and AA254616 to AA25473 represent
 CC PCR primers used in the exemplification of the present invention. The
 CC polypeptides, the polynucleotides, antibodies and compositions of the
 CC invention can be used as vaccines, as diagnostic reagents, and as
 CC immunogenic compositions. The polypeptides can be used in the manufacture
 CC of medicaments for treating or preventing infection due to *Neisserial*
 CC bacteria (e.g. meningitis and septicemia), to detect the presence of
 CC *Neisseria* bacteria, or to raise antibodies. They may also be used to
 CC screen for agonists or antagonists, which may themselves have use as
 CC antibacterial agents. The polynucleotides of the invention may also be
 CC used in gene therapy protocols
 XX
 XX Sequence 948 BP; 244 A; 270 C; 227 G; 207 T; 0 U; 0 Other;
 SQ
 Query Match 93.9%; Score 890.4; DB 3; Length 948;
 Best Local Similarity 96.2%; Pred. No. 1.3e-258;
 Matches 912; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

DB 361 CGTATGGATTGGACAAACGTTGAAAGACGCGACGAAATCAACAGCAGCGCTGTCC 420
 QY 421 GCCCTCGATGAAGCCCGCGGCGCTTGGGTGTGAAGTCTCCGTTAGCAATCAAGAT 480
 DB 421 GCCCTCGATGAAGCCCGCGGCGCTTGGGTGTGAAGTCTCCGTTAGCAATCAAGAT 480
 QY 481 TTGGTTCGCGCGCAAGAAATCCTTGGCGCAATGACGACCAAAATTACCGCGCAAGCA 540
 DB 481 TTGGTTCGCGCGCAAGAAATCCTTGGCGCAATGACGACCAAAATTACCGCGCAAGCA 540
 QY 541 AAACGCGCGCGTATTGCGCAATCCGAAGCGCTGAATAATGAACAATCAACCTTGCAGT 600
 DB 541 AAACGCGCGCGTATTGCGCAATCCGAAGCGCTGAATAATGAACAATCAACCTTGCAGT 600
 QY 601 GGTGACGCGTGAAGCGCAATCCGAAGCGCTGAAGCGCTGAAGCGCTGAAGCGCTGAAG 660
 DB 601 GGTGACGCGTGAAGCGCAATCCGAAGCGCTGAAGCGCTGAAGCGCTGAAGCGCTGAAG 660
 QY 661 TCCATATGCGGCAAGAAATGCGCGCATCAACGCGCGCAAGGCGGCAATCCCTGCGC 720
 DB 661 TCCATATGCGGCAAGAAATGCGCGCATCAACGCGCGCAAGGCGGCAATCCCTGCGC 720
 QY 721 CTGTGTCGGAAGCGCAATGCGCAAGCGCATCCGTCAAATTCGCGCGCTTGAACCGCA 780
 DB 721 CTGTGTCGGAAGCGCAATGCGCAAGCGCATCCGTCAAATTCGCGCGCTTGAACCGCA 780
 QY 781 GCGCGGCGCGATGCGGTCATCTGAAGATTGCGGAACAATAGTCAGCGCGCTTCAACAT 840
 DB 781 GCGCGGCGCGATGCGGTCATCTGAAGATTGCGGAACAATAGTCAGCGCGCTTCAACAT 840
 QY 841 CTTCGCAAGAAAGCAATCGCTGATTATGCGCGCAATGTTGCGGACATCGGACGCTG 900
 DB 841 CTTCGCAAGAAAGCAATCGCTGATTATGCGCGCAATGTTGCGGACATCGGACGCTG 900
 QY 901 ATTTGCGCGCGATGAATAATTATCGACAGCAGCAAAACCGCCAAATTA 948
 DB 901 ATTTGCGCGCGATGAATAATTATCGACAGCAGCAAAACCGCCAAATTA 948

RESULT 10
 AAAB1268
 ID AAAB1268 standard; DNA; 948 BP.

XX AAAB1268;

XX 04-DEC-2000 (first entry)

DE N. meningitidis partial DNA sequence a519-1.seq SEQ ID NO:978.

XX *Neisseria meningitidis*; *Neisseria gonorrhoeae*; genome; immunogenic;
 KW antigen; vaccine; diagnosis; infection; antibacterial; identification;
 KM *Meningococcus B*; MenB; de.

XX *Neisseria meningitidis*.

XX MO200022430-A2.

XX 20-APR-2000.

PF 08-OCT-1999; 99WO-US023573.

XX 09-OCT-1998; 98US-0103794P.

PR 30-APR-1999; 99US-0132068P.

XX (CHIR) CHIRON CORP.

XX Frazer CM, Hickey E, Petersen J, Tettelin H, Venter JC,
 PI Maignani V, Galeotti C, Mora M, Ratti G, Scarselli M,
 PI Rappuoli R, Pizsa M;
 XX
 DR WPI: 2000-318079/27.
 DR P-PSDB; AAB25628.

specifically obtained *Neisseria meningitidis* genomic DNA sequences; CC
 CC AAA81260 to AAA81303 and AAB25620 to AAB25663 represent *Neisseria* DNA
 CC sequences and their corresponding proteins; AAA81254 to AAA81259 and
 CC AAA81304 to AAA81321 represent PCR primers used in the isolation of
 CC *Neisseria meningitidis* DNA sequences; and AAA81322 to AAA81452 represent
 CC *Neisseria meningitidis* Msp polymucleotide ODF sequences, which are all
 CC used in the exemplification of the present invention. The nucleic acid
 CC sequences, protein sequences, and antibodies against them, can be used in
 CC the manufacture of a composition. The composition can be used as a
 CC medicament (or in the manufacture of a medicament) for treating,
 CC preventing or diagnosing infection due to *Neisseria* bacteria. For
 CC example, some of the identified proteins could be components of vaccines
 CC against *Meningococcus B*; against all serotypes; and/or against all
 CC pathogenic *Neisseriae*. Identification of sequences from the bacterium
 CC will also facilitate production of biological probes, particularly
 CC organism-specific probes. Attempts to make efficacious *Meningococcus B*
 CC vaccines have failed mainly due to antigen tolerance. Multivalent
 CC vaccines have also been tried but none have successfully overcome
 CC antigenic variability. The provision of further, complete sequences may
 CC provide an opportunity to identify secreted or surface exposed proteins
 CC that may be presumed targets for the immune system and which are not
 CC antigenically variable or at least more conserved than other more
 CC variable regions

XX Sequence 948 BP; 244 A; 270 C; 227 G; 207 T; 0 U; 0 Other;
 SO
 Query Match 93.9%; Score 890.4; DB 3; Length 948;
 Best Local Similarity 96.2%; Pred. No. 1.3e-258;
 Matches 912; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 ATGGAAATTTTCTTATCTTGTGGAGCCGCGCTTGGCGTTCAATCTTGTTC 60
 DB 1 ATGGAAATTTTCTTATCTTGTGGAGCCGCGCTTGGCGTTCAATCTTGTTC 60
 QY 61 GTCATCCCGAGAGAGAGTCACGTTGCGAAAGGCTGGGCGTTCCATCGCGCCG 120
 DB 61 GTCATCCCGAGAGAGAGTCACGTTGCGAAAGGCTGGGCGTTCCATCGCGCCG 120
 QY 121 ACGGCCGGTTGAAATTTTGTATCCCTTTATGACCGCGCTGCTACCGCCATTGCTG 180
 DB 121 ACGGCCGGTTGAAATTTTGTATCCCTTTATGACCGCGCTGCTACCGCCATTGCTG 180
 QY 181 AAAAGAAATCCCTTTAAGCAGTACCGACGAGTTCATCAGCGCGCATATAGCAATTG 240
 DB 181 AAAAGAAATCCCTTTAAGCAGTACCGACGAGTTCATCAGCGCGCATATAGCAATTG 240
 QY 241 ACTGTTGAGGAGTCAATCTATTTCCAAAGTACCGATCCCAATCGCTCATAGCGTTG 300
 DB 241 ACTGTTGAGGAGTCAATCTATTTCCAAAGTACCGATCCCAATCGCTCATAGCGTTG 300
 QY 301 AGCAATCACTATGCAATTAATCCAGCTTGCCCAACAGCGCTGCGTTCCGTTATCGAG 360
 DB 301 AGCAATCACTATGCAATTAATCCAGCTTGCCCAACAGCGCTGCGTTCCGTTATCGAG 360
 QY 361 CGTATGAGTGTGACAAACGTTTGAAGAAAGCGGCAAAATCAACAGTACGCTGCTCC 420
 DB 361 CGTATGAGTGTGACAAACGTTTGAAGAAAGCGGCAAAATCAACAGTACGCTGCTCC 420
 QY 421 GCCCTGATGAAACCGCGGAGCTTGGGGGTGAAAGTCTCCGTTACGAATCAAGAGAT 480
 DB 421 GCCCTGATGAAACCGCGGAGCTTGGGGGTGAAAGTCTCCGTTACGAATCAAGAGAT 480
 QY 481 TTGGTTCGCGCGCAAGAAATCTTGGCGCAATGACGAGCACAATTCGCGCAAGCGAA 540
 DB 481 TTGGTTCGCGCGCAAGAAATCTTGGCGCAATGACGAGCACAATTCGCGCAAGCGAA 540
 QY 541 AAAAGCGCCCGTATTCGCGCAATCGAAGCGCGTAAATTCGAACAAATCAACTTGGCAGT 600
 DB 541 AAAAGCGCCCGTATTCGCGCAATCGAAGCGCGTAAATTCGAACAAATCAACTTGGCAGT 600
 QY 601 GGTGAGGTGAAGCCGAATTCGAACCAATTCGAAGGCGAGGCTCAGGCTGGGTCATGCG 660
 DB 601 GGTGAGGTGAAGCCGAATTCGAACCAATTCGAAGGCGAGGCTCAGGCTGGGTCATGCG 660

QY 661 TCCAATGCCGAGAAATCGCCGCGCATCAACGCGCCCAAGCGAAGCGAAATCCCTGCGC 720
 DB 661 TCCAATGCCGAGAAATCGCCGCGCATCAACGCGCCCAAGCGAAGCGAAATCCCTGCGC 720
 QY 721 CTTGTTGGCGAAGCCCAATGCGCAAGCCATTCGCTCAATTTGCGCGCCCTTCAACCCAA 780
 DB 721 CTTGTTGGCGAAGCCCAATGCGCAAGCCATTCGCTCAATTTGCGCGCCCTTCAACCCAA 780
 QY 781 GCGCGGGGAGATGCGGCTCAATTCGAAGATTCGGGAACAATTCGTAGCCGCTTCAACAT 840
 DB 781 GCGCGGTGGAGATGCGGCTCAATTCGAAGATTCGGGAACAATTCGTAGCCGCTTCAACAT 840
 QY 841 CTTGCAAGAAAGCAATACGCTATTAATGCCCCCAATGTTGCCGATCGGACGCTG 900
 DB 841 CTTGCAAGAAAGCAATACGCTATTAATGCCCCCAATGTTGCCGATCGGACGCTG 900
 QY 901 ATTTCTGCGCGCATGAAATTAATTCAGACAGCAAGCAAAACCGCCAAATTA 948
 DB 901 ATTTCTGCGCGCATGAAATTAATTCAGACAGCAAGCAAAACCGCCAAATTA 948

RESULT 12
 AAF21553
 ID AAF21553 standard; DNA; 948 BP.
 XX AAF21553;
 AC
 XX
 DT 13-MAR-2001 (first entry)
 XX
 DE N. meningitidis partial DNA sequence a519-1.seq SEQ ID NO:18.

XX *Neisseria meningitidis*; *Neisseria gonorrhoeae*; immunogenic; vaccine;
 KW diagnosis; antigen; detection; infection; gene therapy; antibacterial;
 KM ds.
 OS *Neisseria meningitidis*.

XX WO200066791-A1.
 XX
 PN 09-NOV-2000.
 PD
 XX
 PF 08-MAR-2000; 2000WO-US005928.
 XX
 PR 30-APR-1999; 99US-013206BP.
 PR 08-OCT-1999; 99WO-US023573.
 PR 28-FEB-2000; 2000GB-00004695.
 XX

PA (CHIR) CHIRON CORP.
 PA (GENO-) INST GENOMIC RES.

XX Pizza M, Hickey B, Peterson J, Tettelein H, Venter JC;
 PI Massimani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scariato V;
 PI Rappuoli R, Frazer CM, Grandi G;
 XX
 DR WPI; 2000-647603/62.
 DR P-PSDB; AAB58558.

PT *Neisseria meningitidis* B full length genome sequence and open reading
 PT frames are used to detect, treat and prevent *Neisseria* infections.
 XX
 PS Example 1; Page 75; 692pp; English.

XX The present invention describes the full length genome of *Neisseria*
 CC meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613
 CC represent fragments of the NMB genomic sequence, as the sequence was too
 CC long to go in a record on its own it was split into 8 sequences which
 CC overlap each other at the beginning and end of each sequence by 4980 bp
 CC (i.e. the last 4980 bp of AAF21544 is repeated at the beginning of
 CC AAF21607, the last 4980 bp of AAF21607 are repeated at the beginning of
 CC AAF21608, and so on). AAF21545 to AAF21588 encode the *Neisseria* proteins
 CC given in AAB58550 to AAB58593, and AAF21589 to AAF21606 represent PCR
 CC primers which are used in the exemplification of the present invention.

CC The NMB genome and fragments from it have antibacterial activity, and can
 CC be used in vaccines and gene therapy. Neisseria nucleic acids, proteins
 CC and/or antibodies which bind to the proteins can be used in compositions
 CC for treating or preventing infection due to Neisserial bacteria or as a
 CC diagnostic reagent for detecting the presence of Neisserial bacteria or
 CC of antibodies raised to Neisserial bacteria. Computer, computer memory,
 CC computer storage medium or computer databases can be used in a search to
 CC identify open reading frames (ORFs) or coding sequences within the NMB
 CC genome. The DNA sequences provide further opportunities to find antigenic
 CC or immunogenic proteins which are more effective in vaccines than the
 CC outer membrane proteins currently used

XX Sequence 948 BP; 244 A; 270 C; 227 G; 207 T; 0 U; 0 Other;

Query Match 93.9%; Score 890.4; DB 3; Length 948;

Best Local Similarity 96.2%; Pred. No. 1.3e-258; Indels 0; Gaps 0;

Matches 912; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 ATGGAATTTTTCATATCTTGTGGAGCGCGCTTGTGGCTTCAAAATCCTTGTG 60
 DB 1 ATGGAATTTTTCATATCTTGTGGAGCGCGCTTGTGGCTTCAAAATCCTTGTG 60
 QY 61 GTGATCCCCCAGAGAAAGTCCAGCTGTGAAAAGCTCGGCTTTCATCGCCCTG 120
 DB 61 GTGATCCCCCAGAGAAAGTCCAGCTGTGAAAAGCTCGGCTTTCATCGCCCTG 120
 QY 121 ACGGCGGTTTGAATTTTGAATCCCTTATCGACCGGTGCGCTACCGCATCGCGT 180
 DB 121 ACGGCGGTTTGAATTTTGAATCCCTTATCGACCGGTGCGCTACCGCATCGCGT 180
 QY 181 AAGAAATCCCTTGTAGACGTACCCAGCCAGCTCTGCATACCGCGATTAATAGCAAT 240
 DB 181 AAGAAATCCCTTGTAGACGTACCCAGCCAGCTCTGCATACCGCGATTAATAGCAAT 240
 QY 241 ACTGTTGACGCGATCATCTATTTCAGAGTAACCGAATCCCAATCTCGCTCATCGCTTG 300
 DB 241 ACTGTTGACGCGATCATCTATTTCAGAGTAACCGAATCCCAATCTCGCTCATCGCTTG 300
 QY 301 AGCAATCATATATAGGCATTTACCAAGCTTGGCCAAAGACGCTGCTTATCGGG 360
 DB 301 AGCAATCATATATAGGCATTTACCAAGCTTGGCCAAAGACGCTGCTTATCGGG 360
 QY 361 CGTATGAGATTGAGCAAAAGCTTTGAGAACGCGCAAGAAATCAACGACCGTCTG 420
 DB 361 CGTATGAGATTGAGCAAAAGCTTTGAGAACGCGCAAGAAATCAACGACCGTCTG 420
 QY 421 GCCCTCGATGAAGCGCGCGGCTTGGGGTGTGAAGTCTTCGTTACGAATCAAGAT 480
 DB 421 GCCCTCGATGAAGCGCGCGGCTTGGGGTGTGAAGTCTTCGTTACGAATCAAGAT 480
 QY 481 TTGGTTCCGCGCGCAAGAAATCTTGGCGGAATGCGGCAATTAACCGCGCAAGCGGA 540
 DB 481 TTGGTTCCGCGCGCGCAAGAAATCTTGGCGGAATGCGGCAATTAACCGCGCAAGCGGA 540
 QY 541 AAAAGCGCGCGGATTTGCGCAATCCGAAGGCGCTTAATATGACCAATCACTTCCAGT 600
 DB 541 AAAAGCGCGCGGATTTGCGCAATCCGAAGGCGCTTAATATGACCAATCACTTCCAGT 600
 QY 601 GGTGACGCGGATTCGCGCAATCCGAAGGCGCTTAATATGACCAATCACTTCCAGT 660
 DB 601 GGTGACGCGGATTCGCGCAATCCGAAGGCGCTTAATATGACCAATCACTTCCAGT 660
 QY 661 TCCATGCGCGAAGAAATGCGCGCGCATCAACCGCGCGCAAGGCGGAATCCCTGGCG 720
 DB 661 TCCATGCGCGAAGAAATGCGCGCGCATCAACCGCGCGCAAGGCGGAATCCCTGGCG 720
 QY 721 CTTGTTGCGGAGGCAATGCGCGCGCATCAACCGCGCGCGCGCTTCAAAACCGCA 780
 DB 721 CTTGTTGCGGAGGCAATGCGCGCGCATCAACCGCGCGCGCGCTTCAAAACCGCA 780
 QY 781 GCGGCGCGGATGCGGTCATCTGAAGATTTGGGGAACCAATACGTGCGCGCTTCAACAT 840
 DB 781 GCGGCGCGGATGCGGTCATCTGAAGATTTGGGGAACCAATACGTGCGCGCTTCAACAT 840

QY 841 CTTGCCAAAGAAACCAATACGCTGATTATGCCCCCAATGTTGGCAGCATCGAGCCTG 900
 DB 841 CTTGCCAAAGAAACCAATACGCTGATTATGCCCCCAATGTTGGCAGCATCGAGCCTG 900
 QY 901 ATTTCTGCGCGCATGAAATTTATGACAGCAGCAAAACCGCGCAATTA 948
 DB 901 ATTTCTGCGCGTATGAAATTTATGACAGCAGCAAAACCGCGCAATTA 948

RESULT 13

AAFP2150
 ID AAFP2150 standard; DNA; 948 BP.

XX AAFP2150;

XX 13-MAR-2001 (first entry)

XX N. meningitidis partial DNA sequence as19.seq SEQ ID NO:12.

XX Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;
 KW diagnosis; antigen; detection; infection; gene therapy; antibacterial;
 KM ds.

XX Neisseria meningitidis.

XX WO200066791-A1.

XX 09-NOV-2000.

XX 08-MAR-2000; 2000WO-US005928.

XX 30-APR-1999; 99US-0132068P.

XX 08-OCT-1999; 99WO-US023573.

XX 28-FEB-2000; 2000GB-00004695.

XX (CHIR) CHIRON CORP.

XX (GENO-) INST GENOMIC RES.

XX Pizsa M, Hickey E, Peterson J, Tettelin H, Venter JC;
 PI Mastragni V, Galeotti C, Mora M, Ratci G, Scarselli M, Scariato V;
 PI Rappuoli R, Frazer CM, Grandi G;

XX WPI; 2000-647603/62.

XX P-PsDB; AAB58555.

XX Neisseria meningitidis B full length genome sequence and open reading
 PT frames are used to detect, treat and prevent Neisserial infections.

XX Example 1; Page 73; 692pp; English.

XX The present invention describes the full length genome of Neisseria
 CC meningitidis B (NMB). The sequences in AAFP21544 and AAFP21607 to AAFP21613
 CC represent fragments of the NMB genomic sequence, as the sequence was too
 CC long to go in a record on its own it was split into 8 sequences which
 CC overlap each other at the beginning and end of each sequence by 49980 bp
 CC (i.e. the last 49980 bp of AAFP21544 is repeated at the beginning of
 CC AAFP21607, the last 49980 bp of AAFP21607 are repeated at the beginning of
 CC AAFP21608, and so on). AAFP21545 to AAFP21588 encode the Neisseria proteins
 CC given in AAB58550 to AAB58593, and AAFP21589 to AAFP21606 represent PCR
 CC primers which are used in the exemplification of the present invention.
 CC The NMB genome and fragments from it have antibacterial activity, and can
 CC be used in vaccines and gene therapy. Neisseria nucleic acids, proteins
 CC and/or antibodies which bind to the proteins can be used in compositions
 CC for treating or preventing infection due to Neisserial bacteria or as a
 CC diagnostic reagent for detecting the presence of Neisserial bacteria or
 CC of antibodies raised to Neisserial bacteria. Computers, computer memory,
 CC computer storage medium or computer databases can be used in a search to
 CC identify open reading frames (ORFs) or coding sequences within the NMB
 CC genome. The DNA sequences provide further opportunities to find antigenic
 CC or immunogenic proteins which are more effective in vaccines than the
 CC outer membrane proteins currently used

QY 121 ACGCCGGTTGAAATATTTGATTCCTTTATGACCGCGTGCCTACCGCATTCGCTG 180
 DB 121 ACGCCGGTTGAAATATTTGATTCCTTTATGACCGCGTGCCTACCGCATTCGCTG 180
 QY 181 AAAAATATCCCTTTAGAGTACCCAGCGGTCTGATCAAGCGGATTAATACCAATTG 240
 DB 181 AAAAATATCCCTTTAGAGTACCCAGCGGTCTGATCAAGCGGATTAATACCAATTG 240
 QY 241 ACTGTGACGCGATCATCTATTTCCAAAGTAAACCGATCCCAACTGCGCTCATACGGTTG 300
 DB 241 ACTGTGACGCGATCATCTATTTCCAAAGTAAACCGATCCCAACTGCGCTCATACGGTTG 300
 QY 301 AGCAATACATTTATGCAATTAACCAAGCTTCCCAAGCGGTGCGTTCCGTTATCGGG 360
 DB 301 AGCAATACATTTATGCAATTAACCAAGCTTCCCAAGCGGTGCGTTCCGTTATCGGG 360
 QY 361 CGTATGAGTTGACAAAACGTTGAGAGACCGACCAATCAACAGTACGTCCTCC 420
 DB 361 CGTATGAGTTGACAAAACGTTGAGAGACCGACCAATCAACAGTACGTCCTCC 420
 QY 421 GCCCTCGATGAGCGCGCGGGGCTTGGGGTGTGAAGGCTCCGTTACGAATCAAGGAT 480
 DB 421 GCCCTCGATGAGCGCGCGGGGCTTGGGGTGTGAAGGCTCCGTTACGAATCAAGGAT 480
 QY 481 TTGGTTCCGCGCGCAAGAAATCTTCGCGCAATGACGACCAATTAACCGCGAAACGCGAA 540
 DB 481 TTGGTTCCGCGCGCAAGAAATCTTCGCGCAATGACGACCAATTAACCGCGAAACGCGAA 540
 QY 541 AAAGCGCGCGTATTTGCGCAATCCGAAAGCGGTAAATCGAACCAATACCTTGCCAGT 600
 DB 541 AAAGCGCGCGTATTTGCGCAATCCGAAAGCGGTAAATCGAACCAATACCTTGCCAGT 600
 QY 601 GGTGAGCGTGAAGCGCAATCAATCCGAAAGCGGTGCGGTGCGGTCAATGCG 660
 DB 601 GGTGAGCGTGAAGCGCAATCAATCCGAAAGCGGTGCGGTGCGGTCAATGCG 660
 QY 661 TCCATGCGCGCAAGAAATCGCCGATCAACCGCGCAAGCGCAAGCGCAATCCCTGCGC 720
 DB 661 TCCATGCGCGCAAGAAATCGCCGATCAACCGCGCAAGCGCAAGCGCAATCCCTGCGC 720
 QY 721 CTGTGCGCGCAAGCAATGCGCAAGCGCATCCGTCATTAATGCGCGCGCTTCAACCCAA 780
 DB 721 CTGTGCGCGCAAGCAATGCGCAAGCGCATCCGTCATTAATGCGCGCGCTTCAACCCAA 780
 QY 781 GCGCGCGCGATGCGGTCAATCTGAAGTTGCGGAACATGCGGCGGTGCAACAT 840
 DB 781 GCGCGCGCGATGCGGTCAATCTGAAGTTGCGGAACATGCGGCGGTGCAACAT 840
 QY 841 CTGTGCGCAAGCAATGCGGTATTTGCGCGCAATGTTGCGCATCGGACGCTG 900
 DB 841 CTGTGCGCAAGCAATGCGGTATTTGCGCGCAATGTTGCGCATCGGACGCTG 900
 QY 901 A-TTTTGTGCGGATGAAATTAATGACAGCAGCAAAACCGCCAA 945
 DB 901 AATTTTGTGCGGATGAAATTAATTTTGTGCGCAGAGCAAAACCGCCAA 947

RESULT 15
 ID AAA81264 standard; DNA; 951 BP.
 AC AAA81264;
 XX
 DT 15-SEP-2003 (revised)
 DT 04-DEC-2000 (first entry)
 XX
 DE N. gonorrhoeae partial DNA sequence g519.seq SEQ ID NO:970.
 XX
 KW Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;
 KM antigen; vaccine; diagnosis; infection; antibacterial; identification;
 XX Meningococcus B; Memb; ds.

OS Neisseria gonorrhoeae.
 XX
 XX WO200022430-A2.
 XX
 XX 20-APR-2000.
 XX
 XX 08-OCT-1999; 99WO-US023573.
 XX
 XX 09-OCT-1998; 98US-0103794P.
 PR 30-APR-1999; 99US-0132068P.
 XX
 XX (CHIR) CHIRON CORP.
 XX
 XX Frazer CM, Hickey E, Peterson J, Tetzelin H, Venter JC, Masiagnani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V, Rapuoli R, Pizzo M;
 DR WPI; 2000-318079/27.
 DR P-PSDB; AAB25624.
 XX
 PT Isolated nucleotide sequences of Neisseria meningitidis which can be used
 PT in the diagnosis and treatment of N. meningitidis infection and other
 PT Neisserial infections, for example, N.gonorrhoea.
 XX
 PS Claim 9; Page 71; 1760pp; English.
 XX
 XX The present invention describes methods of obtaining immunogenic proteins
 CC from Neisseria genomic sequences. AAA81453 to AAA82414 represent
 CC specifically claimed Neisseria meningitidis genomic DNA sequences;
 CC AAA81460 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DNA
 CC sequences and their corresponding proteins; AAA81254 to AAA81259 and
 CC AAA81304 to AAA81321 represent PCR primers used in the isolation of
 CC Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent
 CC Neisseria meningitidis Memb polynucleotide ORF sequences, which are all
 CC used in the exemplification of the present invention. The nucleic acid in
 CC sequences, protein sequences, and antibodies against them, can be used in
 CC the manufacture of a composition. The composition can be used as a
 CC medicament (or in the manufacture of a medicament) for treating, for
 CC preventing or diagnosing infection due to Neisserial bacteria. For
 CC example, some of the identified proteins could be components of vaccines
 CC against Meningococcus B; against all serotypes; and/or against all
 CC pathogenic Neisseriae. Identification of sequences from the bacterium
 CC will also facilitate production of biological probes, particularly
 CC organism-specific probes. Attempts to make efficacious Meningococcus B
 CC vaccines have failed mainly due to antigen tolerance. Multivalent
 CC vaccines have also been tried but none have successfully overcome
 CC antigenic variability. The provision of further, complete sequences may
 CC provide an opportunity to identify secreted or surface exposed proteins
 CC that may be presumed targets for the immune system and which are not
 CC antigenically variable or at least more conserved than other more
 CC variable regions. (Updated on 15-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 951 BP; 252 A; 274 C; 228 G; 197 T; 0 U; 0 Other;
 Query Match 93.5%; Score 886.6; DB 3; Length 951;
 Best Local Similarity 96.7%; Pred. No. 1.9e-257;
 Matches 916; Conservative 0; Mismatches 29; Indels 2; Gaps 1;
 QY 1 ATGGAATTTTTCATTATCTGTTGGACAGCGGTGCGGCTTTTGGCTTCAAAATCCTTTGTC 60
 DB 1 ATGGAATTTTTCATTATCTGTTGGACAGCGGTGCGGCTTTTGGCTTCAAAATCCTTTGTC 60
 QY 61 GTCAATCCCGCAGCAAGTCCAGTGTGAAAGGCTCGGGCGCTTCCATCGGCGCCTG 120
 DB 61 GTCAATCCCGCAGCAAGTCCAGTGTGAAAGGCTCGGGCGCTTCCATCGGCGCCTG 120
 QY 121 ACGCGCGTTTGAATATTTGATTCCTTTATGACCGCGTGCCTACCGCATTCGCTG 180
 DB 121 ACGCGCGTTTGAATATTTGATTCCTTTATGACCGCGTGCCTACCGCATTCGCTG 180
 QY 181 AAAAATATCCCTTTAGAGTACCCAGCGGTCTGATCAAGCGGATTAATACCAATTG 240
 DB 181 AAAAATATCCCTTTAGAGTACCCAGCGGTCTGATCAAGCGGATTAATACCAATTG 240


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Qy 241 ACTGTTGAGCGCATCATTTATTTCCAAAGTAACCGATCCCAAACTGCGCTCATACGCTTCG 300
Db 241 ACTGTTGAGCGCATCATTTATTTCCAAAGTAACCGATCCCAAACTGCGCTCATACGCTTCG 300
Qy 301 AGCAACTATATTAATGGAATTAACCGAGCTTGGCCAAAGAGAGCGCTGCTTCCGTTATCGAG 360
Db 301 AGCAACTATATTAATGGAATTAACCGAGCTTGGCCAAAGAGAGCGCTGCTTCCGTTATCGAG 360
Qy 361 CGATGAGATTGACAAACGTTTGAGAGAGCGGACGGAATCAACAGTACCGTCTCTCC 420
Db 361 CGATGAGATTGACAAACGTTTGAGAGAGCGGACGGAATCAACAGTACCGTCTCTCC 420
Qy 421 GCCCTGATGAGAGCGCGCGGCGCTTGGGCGTGTGAAGTCTCCGTTACGAAATCAAGAT 480
Db 421 GCCCTGATGAGAGCGCGCGGCGCTTGGGCGTGTGAAGTCTCCGTTACGAAATCAAGAT 480
Qy 481 TTGTTTCCGCGCGCAAGAAATCCTTGGCGCAATGACGAGCAAAATTAACGCGGACGCGGA 540
Db 481 TTGTTTCCGCGCGCAAGAAATCCTTGGCGCAATGACGAGCAAAATTAACGCGGACGCGGA 540
Qy 541 AAACGCGCGCGTATTTGCGGAATCCGAGAGCGCGTAATAATCAACATCAACCTTCCAGT 600
Db 541 AAACGCGCGCGTATTTGCGGAATCCGAGAGCGCGTAATAATCAACATCAACCTTCCAGT 600
Qy 601 GGTGAGCGTGAAGCGGAATCCACACATCCGAGAGCGCTGAGGCTGCGGTCAATGCG 660
Db 601 GGTGAGCGTGAAGCGGAATCCACACATCCGAGAGCGGCTGAGGCTGCGGTCAATGCG 660
Qy 661 TTCCATGCGCGAAGAAATGCGCGCGCATCAACGCGCGCAAGAGCGGAATCCGTCGCG 720
Db 661 TTCCATGCGCGAAGAAATGCGCGCGCATCAACGCGCGCAAGAGCGGAATCCGTCGCG 720
Qy 721 CTGTTGCGGAGCAATGCGCGAGCCATCCGTCAAATTTGCGCGCGCTTCAAAACCA 780
Db 721 CTGTTGCGGAGCAATGCGCGAGCCATCCGTCAAATTTGCGCGCGCTTCAAAACCA 780
Qy 781 GCGCGGCGCGATGCGGTCAATCTGAAGATTGCGGGAACAATACGTACGCGCTTCAACAT 840
Db 781 GCGCGGCGCGATGCGGTCAATCTGAAGATTGCGGGAACAATACGTACGCGCTTCAACAT 840
Qy 841 CTGTCGCAAGAAAGCAATACGCTGATTAATGCGCGCAATTTGCGGACATCGGACGCTG 900
Db 841 CTGTCGCAAGAAAGCAATACGCTGATTAATGCGCGCAATTTGCGGACATCGGACGCTG 900
Qy 901 A-TTTCGCGCGCATGAAATTTATCGACAGCAGCAAAACCGCCAA 945
Db 901 AATTTTCGCGCGCATGAAATTTTTCGCGAGAGCAAAACCGCCAA 947

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RESULT 16
AAFP21549
AAFP21549 standard; DNA; 951 BP.

AAFP21549;
15-SEP-2003 (revised)
13-MAR-2001 (first entry)
N. gonorrhoeae partial DNA sequence g519.seq SEQ ID NO:10.
Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;
diagnosis; antigen; detection; infection; gene therapy; antibacterial;
de.
Neisseria gonorrhoeae.
WO200066791-A1.
09-NOV-2000.
08-MAR-2000; 2000WO-US005928.

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PR 30-APR-1999; 99US-0132068P.  
PR 08-OCT-1999; 99WO-US023573.  
PR 28-FEB-2000; 2000GB-00004695.  
PA (CHIR ) INST GENOMIC RES.  
PA (GENO-) INST GENOMIC RES.  
PI Pizsa M, Hickey E, Peterson J, Tettelin H, Venter JC;  
PI Maignani V, Galeotti C, Mora M, Ratti G, Scarbelli M, Scarlato V,  
PI Rappuoli R, Frazer CM, Grandi G;  
DR WPI; 2000-647603/62.  
DR P-PSDB; AAB58554.  
PT Neisseria meningitidis B full length genome sequence and open reading  
PT frames are used to detect, treat and prevent Neisserial infections.  
XX  
XX  
XX Example 1; Page 71-72; 692pp; English.  
CC The present invention describes the full length genome of Neisseria  
CC meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613  
CC represent fragments of the NMB genomic sequence, as the sequence was too  
CC long to go in a record on its own it was split into 8 sequences which  
CC overlap each other at the beginning and end of each sequence by 49980 bp  
CC (i.e. the last 49980 bp of AAF21544 is repeated at the beginning of  
CC AAF21607, the last 49980 bp of AAF21607 are repeated at the beginning of  
CC AAF21608, and so on). AAF21545 to AAF21589 to AAF21606 represent PCR  
CC primers which are used in the exemplification of the present invention.  
CC The NMB genome and fragments from it have antibacterial activity, and can  
CC be used in vaccines and gene therapy. Neisseria nucleic acids, proteins  
CC and/or antibodies which binds to the proteins can be used in compositions  
CC for treating or preventing infection due to Neisserial bacteria or as a  
CC diagnostic reagent for detecting the presence of Neisserial bacteria or  
CC of antibodies raised to Neisserial bacteria. Computers, computer memory,  
CC computer storage medium or computer databases can be used in a search to  
CC identify open reading frames (ORFs) or coding sequences within the NMB  
CC genome. The DNA sequences provide further opportunities to find antigenic  
CC or immunogenic proteins which are more effective in vaccines than the  
CC outer membrane proteins currently used. (Updated on 15-SEP-2003 to  
CC standardise OS field)  
SQ Sequence 951 BP; 252 A; 274 C; 228 G; 197 T; 0 U; 0 Other;  
Query Match 93.5%; Score 886.6; DB 3; Length 951;  
Best Local Similarity 96.7%; Pred. No. 1.9e-257;  
Matches 916; Conservative 0; Mismatches 29; Indels 2; Gaps 1;  
Qy 1 ATGGAATTTTTCATATCTGTTGGCAGCGCGCGGCTTGGGCTCAAAATCCTTGTG 60  
Db 1 ATGGAATTTTTCATATCTGTTGGCAGCGCGCGGCTTGGGCTCAAAATCCTTGTG 60  
Qy 61 GTCATCCGCCAGCAGGAAGTCCAGCTTGTGAAAGGCTCGGCGCTTCCATCGCGCCCTG 120  
Db 61 GTCATCCGCCAGCAGGAAGTCCAGCTTGTGAAAGGCTCGGCGCTTCCATCGCGCCCTG 120  
Qy 121 ACGGCGGTTGGAATATTTTGAATTCCTTTATCGACCGCGTGTGCTTACCGCCATTCGCTG 180  
Db 121 ACGGCGGTTGGAATATTTTGAATTCCTTTATCGACCGCGTGTGCTTACCGCCATTCGCTG 180  
Qy 181 AAGGAATTCCTTTAGAGTACCGCAGCGCTGTCATCAGCGGATATACGCAATTG 240  
Db 181 AAGGAATTCCTTTAGAGTACCGCAGCGCTGTCATCAGCGGATATACGCAATTG 240  
Qy 241 ACTGTTGAGCGCATCATTTTCCAAAGTAACCGATCCCAAACTGCGCTCATACGCTTTCG 300  
Db 241 ACTGTTGAGCGCATCATTTTCCAAAGTAACCGATCCCAAACTGCGCTCATACGCTTTCG 300  
Qy 301 AGCAACTATATTAATGGAATTAACCGAGCTTGGCCAAAGAGAGCGCTGCTTCCGTTATCGAG 360  
Db 301 AGCAACTATATTAATGGAATTAACCGAGCTTGGCCAAAGAGAGCGCTGCTTCCGTTATCGAG 360  
Qy 361 CGATGAGATTGACAAACGTTTGAGAGAGCGGACGGAATCAACAGTACCGTCTCTCC 420

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Db 361 CGTATGAGTTGACAAAGCTTTGAGAGACGCCAGCAATCAACAGTACGTCTCC 420
Qy 421 GCCCTCATGAAAGCCCGCGGCTTTGGGCTGTAAAGTCTCCGTTACGAATCAAGAT 480
Db 421 GCCCTCATGAAAGCCCGCGGCTTTGGGCTGTAAAGTCTCCGTTACGAATCAAGAT 480
Qy 481 TTGGTTCGCGCGCAAGAAATCCTTCGCGCAATGACGAGCAAAATTACCGCGCAAGCGGAA 540
Db 481 TTGGTTCGCGCGCAAGAAATCCTTCGCGCAATGACGAGCAAAATTACCGCGCAAGCGGAA 540
Qy 541 AAACGCGCCGCTATTTGCGCAATCCGAAGCCGTAATAATCGAACAATCAACCTTCCAGT 600
Db 541 AAACGCGCCGCTATTTGCGCAATCCGAAGCCGTAATAATCGAACAATCAACCTTCCAGT 600
Qy 601 GGTCAAGCTGAAGCCGCAAAATTCACAAATCCCAAGCGGCTCAGGCTGCGGTCAATGCG 660
Db 601 GGTCAAGCTGAAGCCGCAAAATTCACAAATCCCAAGCGGCTCAGGCTGCGGTCAATGCG 660
Qy 661 TCCATGCGCGAAGAAATCGCCGATCAACGCGCAAGCGCAAGCGAATCCCTGCGC 720
Db 661 TCCATGCGCGAAGAAATCGCCGATCAACGCGCAAGCGCAAGCGAATCCCTGCGC 720
Qy 721 CTTGTTGCGCAAGCCCAATGCGCAAGCCATCCGTCAAATTGCGCGCCCTTCAAAACCGAA 780
Db 721 CTTGTTGCGCAAGCCCAATGCGCAAGCCATCCGTCAAATTGCGCGCCCTTCAAAACCGAA 780
Qy 781 GCGCGCGCGATGCGGTCAATCTGAAGATTGCGCAATCTGAAGCGGCTTCAACAT 840
Db 781 AGCGGGGCGATGCGGTCAATCTGAAGATTGCGCAATCTGAAGCGGCTTCAACAT 840
Qy 841 CTTGCCAAGAAAGCAATACGCTGATTTATGCGCGCAATGTTGCGCAATCGGACGCTG 900
Db 841 CTTGCCAAGAAAGCAATACGCTGATTTATGCGCGCAATGTTGCGCAATCGGACGCTG 900
Qy 901 A-TTTGTCGCGCATGAAATTTATCGACAGCAAGAAACCGCCAA 945
Db 901 AATTTTGGCGCATGAAATTTTTCGCAAGCAAGAAACCGCCAA 947

RESULT 17
AAZ53753
ID AAZ53753 standard; DNA; 948 BP.
XX
AC AAZ53753;
XX
DT 21-MAR-2000 (first entry)
XX
DE Neisseria meningitidis ORF 519 partial DNA sequence SEQ ID NO:1455.
XX
KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
KW antibacterial; gene therapy; ds.
XX
OS Neisseria meningitidis.
XX
PN WO9957280-A2.
XX
PD 11-NOV-1999.
XX
PF 30-APR-1999; 99WO-US009346.
XX
PR 01-MAY-1998; 98US-0083758P.
PR 31-JUL-1998; 98US-0094869P.
PR 02-SEP-1998; 98US-0098994P.
PR 02-SEP-1998; 98US-0099062P.
PR 09-OCT-1998; 98US-0103749P.
PR 09-OCT-1998; 98US-0103794P.
PR 09-OCT-1998; 98US-0103796P.
PR 25-FEB-1999; 99US-0121528P.
XX
PA (CHIR ) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
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XX
PI Fraser C, Galeotti C, Grandi G, Hickey E, Maignani V, Mora M,
PI Peteren J, Pizsa M, Rappuoli R, Ratti G, Scalato E, Scarselli M,
PI Tettein H, Venter UC;
XX
DR WPI; 2000-062150/05.
DR P-PSDB; AAY74991.
XX
PT Novel Neisserial polypeptides predicted to be useful antigens for
PT vaccines and diagnostics.
XX
PS Claim 7; Page 779; 1453pp; English.
XX
AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941
CC represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides
CC and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55473 represent
CC PCR primers used in the exemplification of the present invention. The
CC polypeptides, the polynucleotides, antibodies and compositions of the
CC invention can be used as vaccines, as diagnostic reagents, and as
CC immunogenic compositions. The polypeptides can be used in the manufacture
CC of medicaments for treating or preventing infection due to Neisserial
CC bacteria (e.g. meningitis and septicemia), to detect the presence of
CC Neisseria bacteria, or to raise antibodies. They may also be used to
CC screen for agonists or antagonists, which may themselves have use as
CC antibacterial agents. The polynucleotides of the invention may also be
CC used in gene therapy protocols
XX
SQ Sequence 948 BP; 242 A; 261 C; 234 G; 211 T; 0 U; 0 Other;
```

```
Query Match 92.6%; Score 877.6; DB 3; Length 948;
Best local similarity 95.4%; Pred. No. 1e-254;
Matches 904; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
```

```
Qy 1 ATGGAATTTTCAATATCTGTTGGCAGCGGTGCGGTTTTCGCTCAATCCTTGTG 60
Db 1 ATGGAATTTTCAATATCTGTTGGTACCGGTGCGGTTTTCGCTCAATCCTTGTG 60
Qy 61 GTCATCCCCAGCAGAAAGTCCAGTGTGCAAAAGCTCGGCGCTTTCATCGCGCCTG 120
Db 61 GTCATCCCCAGCAGAAAGTCCAGTGTGCAAAAGCTCGGCGCTTTCATCGCGCCTG 120
Qy 121 ACGGCGCGTTGAATATTTGATTCCTTTATCGACCGCGCTTCCATCGGCAATG 180
Db 121 ACGGCGCGTTGAATATTTGATTCCTTTATCGACCGCGCTTCCATCGGCAATG 180
Qy 181 AAAGAAATCCCTTAGAGCTAACCCAGCGGTGCAATCGCGGATTAATAGCAATG 240
Db 181 AAAGAAATCCCTTAGAGCTAACCCAGCGGTGCAATCGCGGATTAATAGCAATG 240
Qy 241 ACTGTTACGCGCATCATCTATTTCCAAAGTAACCGATCCAAATCGGCTCATACGTTG 300
Db 241 ACTGTTACGCGCATCATCTATTTCCAAAGTAACCGATCCAAATCGGCTCATACGTTG 300
Qy 301 AGCAACTACATTAATGAGCAATTAACCGAGTTCGCCAAACGACGCTGCTTATGCGG 360
Db 301 AGCAACTACATTAATGAGCAATTAACCGAGTTCGCCAAACGACGCTGCTTATGCGG 360
Qy 361 CGTATGAGTTGACAAAGGTTTGAAGAACGCGAGCAAAATCAACAGTACGCTCTCC 420
Db 361 CGTATGAGTTGACAAAGGTTTGAAGAACGCGAGCAAAATCAACAGTACGCTCTCC 420
Qy 421 GCCCTCATGAAAGCCCGCGGCTTTGGGCTGTAAAGTCTCCGTTACGAATCAAGAT 480
Db 421 GCCCTCATGAAAGCCCGCGGCTTTGGGCTGTAAAGTCTCCGTTACGAATCAAGAT 480
Qy 481 TTGGTTCGCGCGCAAGAAATCTTCGCGCAATGACGAGCAAAATTACCGCGCAAGCGGAA 540
Db 481 TTGGTTCGCGCGCAAGAAATCTTCGCGCAATGACGAGCAAAATTACCGCGCAAGCGGAA 540
Qy 541 AAACGCGCCGCTATTTGCGCAATCCGAAGCCGTAATAATCGAACAATCAACCTTCCAGT 600
Db 541 AAACGCGCCGCTATTTGCGCAATCCGAAGCCGTAATAATCGAACAATCAACCTTCCAGT 600
```

QY 601 GGTCAGCGGAGAGCCGAATCAACATCCGAAGGCGAGGCTCAGGCTGGGTCATGCG 660
 DB 601 GGTCAGCGGAGAGCCGAATCAACATCCGAAGGCGAGGCTCAGGCTGGGTCATGCG 660
 QY 661 TCCAAATGCGAGAAATCGCCGATCAACCGCGCCAAAGCGAAAGCGAATCCTGCGC 720
 DB 661 TCAAAATGCGAGAAATCGCCGATCAACCGCGCCAAAGCGAAGCGAATCCTGCGC 720
 QY 721 CTGTGTCGGAAGCCGATGCGAGCGATCCGTAATGTCGCGCGCTTCAAAACCA 780
 DB 721 CTGTGTCGGAAGCCGATGCGAGCGATCCGTAATGTCGCGCGCTTCAAAACCA 780
 QY 781 GCGCGGCGGAGATGCGATCAATGGAAGTGGGAACATATAGCGCGCTTCAACAT 840
 DB 781 GCGCGGCGGAGATGCGATCAATGGAAGTGGGAACATATAGCGCGCTTCAACAT 840
 QY 841 CTGTCGCAAGAAAGCAATACGCTGATTAATGCGCCCAATGTCGCGACATCGGCGCTG 900
 DB 841 CTGTCGCAAGAAAGCAATACGCTGATTAATGCGCCCAATGTCGCGACATCGGCGCTG 900
 QY 901 ATTTCTGCGCGATGAAATTAATGACAGACGAAACCGCCCAATTA 948
 DB 901 ATTTCTGCGCGATGAAATTAATGACAGACGAAACCGCCCAATTA 948

RESULT 18
 AA254583
 ID AA254583 standard; DNA; 948 BP.
 AC AA254583;
 DT 21-MAR-2000 (first entry)
 DX Neisseria meningitidis ORF 519 partial DNA sequence SEQ ID NO:3051.
 XX Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
 KM antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
 KM antibacterial; gene therapy; ds.
 OS Neisseria meningitidis.
 XX
 PN WO957280-A2.
 PD 11-NOV-1999.
 XX
 PF 30-APR-1999; 99WO-US009346.
 PR 01-MAY-1998; 98US-0083758P.
 PR 31-JUL-1998; 98US-0094869P.
 PR 02-SEP-1998; 98US-0098994P.
 PR 02-SEP-1998; 98US-0099062P.
 PR 09-OCT-1998; 98US-0103749P.
 PR 09-OCT-1998; 98US-0103794P.
 PR 09-OCT-1998; 98US-0103796P.
 PR 25-FEB-1999; 99US-0121528P.
 XX
 PA (CHIR) CHIRON CORP.
 PA (GENO-) INST GENOMIC RES.
 XX
 PI Frazer C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;
 PI Petersen U, Pizzo M, Rappelli R, Ratti G, Scalato E, Scarselli M;
 PI Tettelein H, Venter JC;
 XX
 DR WPI: 2000-062150/05.
 DR P-PsDB; AAY75781.
 XX
 PT Novel Neisserial polypeptides predicted to be useful antigens for
 PT vaccines and diagnostics.
 XX
 PS Example 1; Page 76; 1453pp; English.
 CC AA253015 to AA254536, AA254577 to AA254615, and AAY74253 to AAY75941
 CC represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides

CC and polypeptides. AA254537 to AA254576 and AA254616 to AA25473 represent
 CC PCR primers used in the exemplification of the present invention. The
 CC polypeptides, the polynucleotides, antibodies and compositions of the
 CC invention can be used as vaccines, as diagnostic reagents, and as
 CC immunogenic compositions. The polypeptides can be used in the manufacture
 CC of medicaments for treating or preventing infection due to Neisserial
 CC bacteria (e.g. meningitis and septicemia), to detect the presence of
 CC Neisseria bacteria, or to raise antibodies. They may also be used to
 CC screen for agonists or antagonists, which may themselves have use as
 CC antibacterial agents. The polynucleotides of the invention may also be
 CC used in gene therapy protocols
 XX
 SQ Sequence 948 BP; 242 A; 261 C; 234 G; 211 T; 0 U; 0 Other;
 Query Match 92.6%; Score 877.6; DB 3; Length 948;
 Best Local Similarity 95.4%; Pred. No. 1e-254;
 Matches 904; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
 QY 1 ATGGAATTTTTCATATCTGTTGGACGCGCGCTTTCGCTTCAATCTTTGTC 60
 DB 1 ATGGAATTTTTCATATCTGTTGGACGCGCGCTTTCGCTTCAATCTTTGTC 60
 QY 61 GTCATCCCCAGACAGAAATCCAGTGTGAAAGCTCGGCGTTTCATCGCGCTG 120
 DB 61 GTCATCCCCAGACAGAAATCCAGTGTGAAAGCTCGGCGTTTCATCGCGCTG 120
 QY 61 GTCATCCCCAGACAGAAATCCAGTGTGAAAGCTCGGCGTTTCATCGCGCTG 120
 DB 61 GTCATCCCCAGACAGAAATCCAGTGTGAAAGCTCGGCGTTTCATCGCGCTG 120
 QY 121 ACGCGCGGTTGAAATTTTGAATTCCTTTATGACCGCGGTGCTTACCGCATTCGCTG 180
 DB 121 ACGCGCGGTTGAAATTTTGAATTCCTTTATGACCGCGGTGCTTACCGCATTCGCTG 180
 QY 121 ACGCGCGGTTGAAATTTTGAATTCCTTTATGACCGCGGTGCTTACCGCATTCGCTG 180
 DB 121 ACGCGCGGTTGAAATTTTGAATTCCTTTATGACCGCGGTGCTTACCGCATTCGCTG 180
 QY 181 AAGAAATCCCTTTAGAGTACCCAGACGCTGTCATACGCGGATTAAGCAATG 240
 DB 181 AAGAAATCCCTTTAGAGTACCCAGACGCTGTCATACGCGGATTAAGCAATG 240
 QY 181 AAGAAATCCCTTTAGAGTACCCAGACGCTGTCATACGCGGATTAAGCAATG 240
 DB 181 AAGAAATCCCTTTAGAGTACCCAGACGCTGTCATACGCGGATTAAGCAATG 240
 QY 241 ACTGTGACGCGCATCATTTTCCAGTAACGATCCCAATCGCTCATACGCTTG 300
 DB 241 ACTGTGACGCGCATCATTTTCCAGTAACGATCCCAATCGCTCATACGCTTG 300
 QY 241 ACTGTGACGCGCATCATTTTCCAGTAACGATCCCAATCGCTCATACGCTTG 300
 DB 241 ACTGTGACGCGCATCATTTTCCAGTAACGATCCCAATCGCTCATACGCTTG 300
 QY 301 AGCAACTACATTAATGCAATTAACCAAGCTTGGCCAAAGACGCTGCTTATCGGG 360
 DB 301 AGCAACTACATTAATGCAATTAACCAAGCTTGGCCAAAGACGCTGCTTATCGGG 360
 QY 301 AGCAACTACATTAATGCAATTAACCAAGCTTGGCCAAAGACGCTGCTTATCGGG 360
 DB 301 AGCAACTACATTAATGCAATTAACCAAGCTTGGCCAAAGACGCTGCTTATCGGG 360
 QY 361 CGTATGAGTGGACAAACGTTTGAAGACGCGCAATCAAGTACCGCTGCTC 420
 DB 361 CGTATGAGTGGACAAACGTTTGAAGACGCGCAATCAAGTACCGCTGCTC 420
 QY 361 CGTATGAGTGGACAAACGTTTGAAGACGCGCAATCAAGTACCGCTGCTC 420
 DB 361 CGTATGAGTGGACAAACGTTTGAAGACGCGCAATCAAGTACCGCTGCTC 420
 QY 421 GCGCTGATGAAGCGCGCGGCTTGGGCTGTAAGTCTCTGTTACGAATCAAGAT 480
 DB 421 GCGCTGATGAAGCGCGCGGCTTGGGCTGTAAGTCTCTGTTACGAATCAAGAT 480
 QY 421 GCGCTGATGAAGCGCGCGGCTTGGGCTGTAAGTCTCTGTTACGAATCAAGAT 480
 DB 421 GCGCTGATGAAGCGCGCGGCTTGGGCTGTAAGTCTCTGTTACGAATCAAGAT 480
 QY 481 TTGTTTCGCGCGCAAGAAATCTTGGCGCATGACGCAATTAACGCGCAAGCA 540
 DB 481 TTGTTTCGCGCGCAAGAAATCTTGGCGCATGACGCAATTAACGCGCAAGCA 540
 QY 481 TTGTTTCGCGCGCAAGAAATCTTGGCGCATGACGCAATTAACGCGCAAGCA 540
 DB 481 TTGTTTCGCGCGCAAGAAATCTTGGCGCATGACGCAATTAACGCGCAAGCA 540
 QY 541 AAACGCGCGCGTATGCGCAATCCGAAGCGCTTAAATGGAACAATCAACCTGCA 600
 DB 541 AAACGCGCGCGTATGCGCAATCCGAAGCGCTTAAATGGAACAATCAACCTGCA 600
 QY 541 AAACGCGCGCGTATGCGCAATCCGAAGCGCTTAAATGGAACAATCAACCTGCA 600
 DB 541 AAACGCGCGCGTATGCGCAATCCGAAGCGCTTAAATGGAACAATCAACCTGCA 600
 QY 601 GGTCAGCGTGAAGCGGAATCCAAATCCGAAGCGAGGCTCAGGCTGCGTCAATGCG 660
 DB 601 GGTCAGCGTGAAGCGGAATCCAAATCCGAAGCGAGGCTCAGGCTGCGTCAATGCG 660
 QY 601 GGTCAGCGTGAAGCGGAATCCAAATCCGAAGCGAGGCTCAGGCTGCGTCAATGCG 660
 DB 601 GGTCAGCGTGAAGCGGAATCCAAATCCGAAGCGAGGCTCAGGCTGCGTCAATGCG 660
 QY 661 TCCAAATGCGAGAAATGCGCGCATCAACCGCGCCAAAGCGAAAGCGAATCCTGCGC 720
 DB 661 TCCAAATGCGAGAAATGCGCGCATCAACCGCGCCAAAGCGAAAGCGAATCCTGCGC 720
 QY 661 TCCAAATGCGAGAAATGCGCGCATCAACCGCGCCAAAGCGAAAGCGAATCCTGCGC 720
 DB 661 TCCAAATGCGAGAAATGCGCGCATCAACCGCGCCAAAGCGAAAGCGAATCCTGCGC 720
 QY 721 CTGTGTCGGAAGCCGATGCGAGCGATCCGTAATGTCGCGCGCTTCAAAACCA 780
 DB 721 CTGTGTCGGAAGCCGATGCGAGCGATCCGTAATGTCGCGCGCTTCAAAACCA 780
 QY 721 CTGTGTCGGAAGCCGATGCGAGCGATCCGTAATGTCGCGCGCTTCAAAACCA 780
 DB 721 CTGTGTCGGAAGCCGATGCGAGCGATCCGTAATGTCGCGCGCTTCAAAACCA 780
 QY 781 GCGCGGCGGAGATGCGATCAATGGAAGTGGGAACATATAGCGCGCTTCAACAT 840
 DB 781 GCGCGGCGGAGATGCGATCAATGGAAGTGGGAACATATAGCGCGCTTCAACAT 840

QY 841 CTGGCAAGAAAGCAATACGCTGATTATGCGCCGCAATGTTGGCGACATCGAGCCTG 900
DB 841 CTGGCAAGAAAGCAATACGCTGATTATGCGCCGCAATGTTGGCGACATCGAGCCTG 900
QY 901 ATTTCTGCGCGCATGAAATTTATCGACGACGCAAAACCGCCAAATTA 948
DB 901 ATTTCTGCGCGCATGAAATTTATCGACGACGCAAAACCGCCAAATTA 948

RESULT 19
AAA81266 standard; DNA; 948 BP.
AAA81266;
04-DEC-2000 (first entry)
N. meningitidis partial DNA sequence m519-1.seq SEQ ID NO:974.
Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;
antigen; vaccine; diagnosis; infection; antibacterial; identification;
Meningococcus B; MenB; ds.
Neisseria meningitidis.
WO200022430-A2.
20-APR-2000.
08-OCT-1999; 99WO-US023573.
09-OCT-1998; 98US-0103794P.
30-APR-1999; 99US-0132068P.
(CHIR) CHIRON CORP.
Frazier CM, Hickey E, Peterson J, Tettelin H, Venter JC, Maignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V, Rappuoli R, Pizza M;
WPI; 2000-318079/27.
P-PSDB; AAB25626.
Isolated nucleotide sequences of Neisseria meningitidis which can be used
in the diagnosis and treatment of N. meningitidis infection and other
Neisserial infections, for example, N.gonorrhoea.
Claim 9; Page 73; 1760pp; English.
The present invention describes methods of obtaining immunogenic proteins
from Neisseria genomic sequences. AAA81453 to AAA82414 represent
specifically claimed Neisseria meningitidis genomic DNA sequences;
AAA81260 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DNA
sequences and their corresponding proteins; AAA81254 to AAA81259 and
AAA81304 to AAA81321 represent PCR primers used in the isolation of
Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent
Neisseria meningitidis MenB polynucleotide ORF sequences, which are all
used in the exemplification of the present invention. The nucleic acid
sequences, protein sequences, and antibodies against them, can be used in
the manufacture of a composition. The composition can be used as a
medicament (or in the manufacture of a medicament) for treating, for
preventing or diagnosing infection due to Neisserial bacteria. For
example, some of the identified proteins could be components of vaccines
against Meningococcus B; against all serotypes; and/or against all
pathogenic Neisseriae. Identification of sequences from the bacterium
will also facilitate production of biological probes, particularly
organism-specific probes. Attempts to make efficacious Meningococcus B
vaccines have failed mainly due to antigen tolerance. Multivalent
antigens have also been tried but none have successfully overcome
antigenic variability. The provision of further, complete sequences may
provide an opportunity to identify secreted or surface exposed proteins
that may be presumed targets for the immune system and which are not

CC antigenically variable or at least more conserved than other more
CC variable regions
XX
SQ Sequence 948 BP; 242 A; 261 C; 234 G; 211 T; 0 U; 0 Other;
Query Match 92.6%; Score 877.6; DB 3; Length 948;
Best Local Similarity 95.4%; Pred. No. 1e-254;
Matches 904; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
QY 1 ATGGAATTTTCTATCTGTTGGCAGCGCGCTTTCGAGCTCAATCCTTGTGTC 60
DB 1 ATGGAATTTTCTATCTGTTGGTGGTACCGCTGCGCTTTCGAGCTCAATCCTTGTGTC 60
QY 61 GTCAATCCCGCAGCAGAGAGTCAAGTGTGCGAAAGGCTCGGCGCTTTCATCGGCCCTG 120
DB 61 GTCAATCCCGCAGCAGAGAGTCAAGTGTGCGAAAGGCTCGGCGCTTTCATCGGCCCTG 120
QY 121 ACGGCGGCTTGAATATTTGATTCCCTTTATCGACCGCGCTTCCGCGCATTCGCTG 180
DB 121 ACGGCGGCTTGAATATTTGATTCCCTTTATCGACCGCGCTTCCGCGCATTCGCTG 180
QY 181 AAGAAATCCCTTAGACGTAACCGACGAGTGTGATCAAGCGCGATTAAGCAATTA 240
DB 181 AAGAAATCCCTTAGACGTAACCGACGAGTGTGATCAAGCGCGATTAAGCAATTA 240
QY 241 ACTGTTGACGCGCATCTATATTTCCAAAGTAACCGATCCCAAATCGGCTCATACGTTTCG 300
DB 241 ACTGTTGACGCGCATCTATATTTCCAAAGTAACCGATCCCAAATCGGCTCATACGTTTCG 300
QY 301 AGCAACTACATTATGATGCAATTTACCGAGCTTGCCCAACGACGCTGCTTCCGTTATCGGG 360
DB 301 AGCAACTACATTATGATGCAATTTACCGAGCTTGCCCAACGACGCTGCTTCCGTTATCGGG 360
QY 361 CGTATGAGTTTGACAAAGGTTTGAAGAACGCGACGAAATCAACAGTACGTCGTCCTCC 420
DB 361 CGTATGAGTTTGACAAAGGTTTGAAGAACGCGACGAAATCAACAGTACGTCGTCCTCC 420
QY 421 GCCCTCATGAGAGCGCGCGCGCTTGGGAGTGTGAAGTCTCCGTTACGAATCAAGAGT 480
DB 421 GCTTTGACAGAGCGCGCGCGCTTGGGAGTGTGAAGTCTCCGTTACGAATCAAGAGT 480
QY 481 TTGGTTCCGCGCAGAAATCTTTCGCGCAATGCGACGACCAATTCACCGCGAAACGCGAA 540
DB 481 TTGGTTCCGCGCAGAAATCTTTCGCGCAATGCGACGACGCAATTCACCGCGAAACGCGAA 540
QY 541 AAAGCGCGCTATTTGCGCAATCCGAAGCGGTAAATTCGAACCAATCAACCTTGCCAGT 600
DB 541 AAAGCGCGCTATTTGCGCAATCCGAAGCGGTAAATTCGAACCAATCAACCTTGCCAGT 600
QY 601 GGTGAGCGTGAAGCGCAATTCGAACCAATTCGAAGCGAGGCTCGAGCTGCGTCAATGCG 660
DB 601 GGTGAGCGCGAAGCGCAATTCGAACCAATTCGAAGCGAGGCTCGAGCTGCGTCAATGCG 660
QY 661 TCGAATGCGCGAAGAAATCGCGCGCATCAACCGCGCCAAAGCGCAAGCGGAATCCCTGCGC 720
DB 661 TCGAATGCGCGAAGAAATCGCGCGCATCAACCGCGCCAAAGCGGAATCCCTGCGC 720
QY 721 CTTGTTGCGCAAGCAATGCGCGAATCCGTCGAATTCGCGCGCGCTTCAAAACCAA 780
DB 721 CTTGTTGCGCAAGCAATGCGCGAATCCGTCGAATTCGCGCGCGCTTCAAAACCAA 780
QY 781 GGGCGGCGGATGCGGTCATCTGAGATTGCGGACCAATACGTAAGCGCGTTCACAGAT 840
DB 781 GGGCGGCGGATGCGGTCATCTGAGATTGCGGACCAATACGTAAGCGCGTTCACAGAT 840
QY 841 CTGGCAAGAAAGCAATACGCTGATTATGCGCCGCAATGTTGGCGACATCGAGCCTG 900
DB 841 CTGGCAAGAAAGCAATACGCTGATTATGCGCCGCAATGTTGGCGACATCGAGCCTG 900
QY 901 ATTTCTGCGCGCATGAAATTTATCGACGACGCAAAACCGCCAAATTA 948
DB 901 ATTTCTGCGCGCATGAAATTTATCGACGACGCAAAACCGCCAAATTA 948

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RESULT 20
AAF21551
ID AAF21551 standard; DNA; 948 BP.
XX
AC AAF21551;
XX
DT 13-MAR-2001 (first entry)
XX
XX N. meningitidis partial DNA sequence m519-1.seq SEQ ID NO:14.
XX
KW Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;
KM diagnosis; antigen; detection; infection; gene therapy; antibacterial;
ds.
XX
OS Neisseria meningitidis.
XX
PN WO200066791-A1.
XX
PD 09-NOV-2000.
XX
PF 08-MAR-2000; 2000MO-US005928.
XX
PR 30-APR-1999; 99US-0132068P.
PR 08-OCT-1999; 99WO-US023573.
PR 28-FEB-2000; 2000GB-00004695.
XX
PA (CHIR ) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX
PI Pizza M, Hickey E, Peterson J, Tettein H, Venter JC;
PI Massignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;
PI Rappuoli R, Frazer CM, Grandi G;
XX
XX MPI: 2000-647603/62.
XX
XX P-PDB: AAB58556.
XX
XX Neisseria meningitidis B full length genome sequence and open reading
XX frames are used to detect, treat and prevent Neisserial infections.
XX
XX Example 1; Page 74; 692pp; English.
XX
XX The present invention describes the full length genome of Neisseria
XX meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613
XX represent fragments of the NMB genomic sequence, as the sequence was too
XX long to go in a record on its own it was split into 8 sequences which
XX overlap each other at the beginning and end of each sequence by 49980 bp
XX (i.e. the last 49980 bp of AAF21544 is repeated at the beginning of
XX AAF21607, the last 49980 bp of AAF21607 are repeated at the beginning of
XX AAF21608, and so on). AAF21545 to AAF21588 encode the Neisseria proteins
XX given in AAB58550 to AAB58593, and AAF21589 to AAF21606 represent PCR
XX primers which are used in the exemplification of the present invention.
XX
XX The NMB genome and fragments from it have antibacterial activity, and can
XX be used in vaccines and gene therapy. Neisseria nucleic acids, proteins
XX and/or antibodies which bind to the proteins can be used in compositions
XX for treating or preventing infection due to Neisserial bacteria or as a
XX diagnostic reagent for detecting the presence of Neisserial bacteria or
XX of antibodies raised to Neisserial bacteria. Computers, computer memory,
XX computer storage medium or computer databases can be used in a search to
XX identify open reading frames (ORFs) or coding sequences within the NMB
XX genome. The DNA sequences provide further opportunities to find antigenic
XX or immunogenic proteins which are more effective in vaccines than the
XX outer membrane proteins currently used
XX
XX Sequence 948 BP; 242 A; 261 C; 234 G; 211 T; 0 U; 0 Other;
XX
Query Match 92.6%; Score 877.6; DB 3; Length 948;
Best Local Similarity 95.4%; Pred. No. 1e-254;
Matches 904; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
QY 1 ATCGAATTTTCTTCTTCTTGGAGCGCGCGGTTTGGCGTTCAAAATCCTTGTG 60
DB 1 ATGGAATTTTCTTCTTCTTGTGTGAGCGCGCGGTTTGGCGTTCAAAATCCTTGT 60
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QY 61 GTCAATCCCCCAGAGGAAGTCCAGTTGTCCGAAAGAGCTCGGAGCTTTCATCGCGCCCTG 120
DB 61 GTCAATCCCAAGAGGAAGTCCAGTTGTCCGAAAGAGCTCGGAGCTTTCATCGCGCCCTG 120
QY 121 ACGGCGGTTTGAATATTTTGAATTCCTTTTATCGACGCGTTCGCTTACCGCATTCGCTG 180
DB 121 ACGGCGGTTTGAATATTTTGAATTCCTTTTATCGACGCGTTCGCTTACCGCATTCGCTG 180
QY 181 AAGAAATCCCTTTAGACGTACCCAGCGAGTTCGATCAAGCGGATTAATAGCAATTG 240
DB 181 AAGAAATCCCTTTAGACGTACCCAGCGAGTTCGATCAAGCGGATTAATAGCAATTG 240
QY 241 AAGAAATCCCTTTAGACGTACCCAGCGAGTTCGATCAAGCGGATTAATAGCAATTG 240
DB 241 AAGAAATCCCTTTAGACGTACCCAGCGAGTTCGATCAAGCGGATTAATAGCAATTG 240
QY 241 ACTGTTGACGGATCATCTATTTCCAAAGTAAACGATCCCAAACTGCGCTCATAGCGTTG 300
DB 241 ACTGTTGACGGATCATCTATTTCCAAAGTAAACGATCCCAAACTGCGCTCATAGCGTTG 300
QY 301 AGCAACTACATTATGGAATTAACCAAGCTTGGCCCAAGAGCGTGCCTTATCGAG 360
DB 301 AGCAACTACATTATGGAATTAACCAAGCTTGGCCCAAGAGCGTGCCTTATCGAG 360
QY 361 CGTATGAGTTGAGCAAAACGTTTGAAGAGCGGAGCAATCAAGTACGTTCTCTCC 420
DB 361 CGTATGAGTTGAGCAAAACGTTTGAAGAGCGGAGCAATCAAGTACGTTCTCTCC 420
QY 421 GCCCTCGATGAAAGCGCGCGGCTTGGGGTGTGAAGTCTCGTTAAGAAATCAAGAT 480
DB 421 GCCCTCGATGAAAGCGCGCGGCTTGGGGTGTGAAGTCTCGTTAAGAAATCAAGAT 480
QY 481 TTTGTTGCGCGCAAGAAATCCTTGCAGCAATGACGAGCAAAATTAACGCGCAACGCGAA 540
DB 481 TTTGTTGCGCGCAAGAAATCCTTGCAGCAATGACGAGCAAAATTAACGCGCAACGCGAA 540
QY 541 AAAAGCGCGCGTATTTGCGGAATCCGAGGCGGTAAATCGAAATCAACTTCTGCAAT 600
DB 541 AAAAGCGCGCGTATTTGCGGAATCCGAGGCGGTAAATCGAAATCAACTTCTGCAAT 600
QY 601 GGTGACGCGTGAAGCGGAAATCCCAATTCGAAAGCGAGGCTCAGGCTGCGTCAATGCG 660
DB 601 GGTGACGCGTGAAGCGGAAATCCCAATTCGAAAGCGAGGCTCAGGCTGCGTCAATGCG 660
QY 661 TCCAAATGCGAGAAATCGCCGCGATCAACCGCGCAAAAGCGAAGCGGAATCCTGCGC 720
DB 661 TCCAAATGCGAGAAATCGCCGCGATCAACCGCGCAAAAGCGAAGCGGAATCCTGCGC 720
QY 721 CTTGTTGCGGAAGCAATTCGAGACCATTCGTCAAATTTGCCGCGCTTCAAAACCAA 780
DB 721 CTTGTTGCGGAAGCAATTCGAGACCATTCGTCAAATTTGCCGCGCTTCAAAACCAA 780
QY 781 GCGCGGCGCGATGCGGTCAATTCGAAAGATTTGGGGAACAATAGTACCGCGTTCAACAT 840
DB 781 GCGCGGCGCGATGCGGTCAATTCGAAAGATTTGGGGAACAATAGTACCGCGTTCAACAT 840
QY 841 CTTGCGCAAGAAAGCAATTCGCTGATATGATGATGATGATGATGATGATGATGATGAT 900
DB 841 CTTGCGCAAGAAAGCAATTCGCTGATATGATGATGATGATGATGATGATGATGATGAT 900
QY 901 ATTTTCGCGCGCATGAAATTTATGACAGACAGCAAAACCGCGCAATTA 948
DB 901 ATTTTCGCGCGCATGAAATTTATGACAGACAGCAAAACCGCGCAATTA 948
RESULT 21
AAAB1459
ID AAAB1459 standard; DNA; 56609 BP.
XX
AC AAAB1459;
XX
DT 04-DEC-2000 (first entry)
XX
XX N. meningitidis partial DNA sequence gnm_7 SEQ ID NO:7.
DB Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;
```


Query Match 92.6%; Score 877.6; DB 3; Length 110000;
 Best Local Similarity 95.4%; Pred. No. 8.9e-254;
 Matches 904; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

1 ATGGAATTTTATTTATCTTTGTCAGCGCGCTTTGGCTTCAATCTTTGTC 60
 DB ATGGAATTTTATTTATCTTTGTCAGCGCGCTTTGGCTTCAATCTTTGTC 95611
 61 GTCAATCCCCAGAGAGTCCAGCTTTCGAAAGGCTGGGCGTTTCATCGCCCTG 120
 DB GTCAATCCCCAGAGAGTCCAGCTTTCGAAAGGCTGGGCGTTTCATCGCCCTG 95551
 121 AGGCGCGGTTTGAATTTTGAATTCCTTTATCGACCGGCTCCATCCGCAATCGCTG 180
 DB AGGCGCGGTTTGAATTTTGAATTCCTTTATCGACCGGCTCCATCCGCAATCGCTG 95491
 181 AAGAAATCCCTTTAGACGTACCCAGCCAGCTCTGATCATCGCGCATTAATGCAATTTG 240
 DB AAGAAATCCCTTTAGACGTACCCAGCCAGCTCTGATCATCGCGCATTAATGCAATTTG 95431
 241 ACTGTTGACGGCATCATTAATTTCCAAAGTACCGAATCCGCTTCATACGGTTG 300
 DB ACTGTTGACGGCATCATTAATTTCCAAAGTACCGAATCCGCTTCATACGGTTG 95371
 301 AGCACTACATTTATGGCAATTAACCGCTTGGCCCAAGCGCTGGTCCGTTATCGGG 360
 DB AGCACTACATTTATGGCAATTAACCGCTTGGCCCAAGCGCTGGTCCGTTATCGGG 95311
 361 CGTATGAGTTTGAAGCAAAAGTTGAAGACGGCAAGCAATCAAGTACCGCTCTG 420
 DB CGTATGAGTTTGAAGCAAAAGTTGAAGACGGCAAGCAATCAAGTACCGCTCTG 95251
 421 GGCCTCGATGAAGCCCGCGGCTTGGGTTGAAGGCTCCGTTACGAATCAAGAT 480
 DB GGCCTCGATGAAGCCCGCGGCTTGGGTTGAAGGCTCCGTTACGAATCAAGAT 95191
 481 TTGGTTCCGCGCGAAGAAATCTTGGCGCAATGACGACCAATTAACCGCCGAAGCGGA 540
 DB TTGGTTCCGCGCGAAGAAATCTTGGCGCAATGACGACCAATTAACCGCCGAAGCGGA 95131
 541 AAACGGCGCGGTTTCCGCAATCCGAAGGCGTGAATCAATCAATCTTGGCAAT 600
 DB AAACGGCGCGGTTTCCGCAATCCGAAGGCGTGAATCAATCAATCTTGGCAAT 95071
 601 GGTCACTGTGAAGCCCAATTCGAATCCGAAGGCGCTGAGCTGCGTCAATGCG 660
 DB GGTCACTGTGAAGCCCAATTCGAATCCGAAGGCGCTGAGCTGCGTCAATGCG 95011
 661 TCCATGCGGAGAAATCGCGCGCATCAACCGCGCAAGGCGAAGCGAATCCCTGCGC 720
 DB TCCATGCGGAGAAATCGCGCGCATCAACCGCGCAAGGCGAAGCGAATCCCTGCGC 94951
 721 CTGTGTCGGAAGCAATGCGCAAGCGCATCCGCAATTTGCGCGCCCTTCAACCCGA 780
 DB CTGTGTCGGAAGCAATGCGCAAGCGCATCCGCAATTTGCGCGCCCTTCAACCCGA 94891
 781 GCGCGGCGGATCGGTCAATCTGAAGATTGCGGAACAATACGTAGCCGCTTCAACAT 840
 DB GCGCGGCGGATCGGTCAATCTGAAGATTGCGGAACAATACGTAGCCGCTTCAACAT 94831
 841 CTGTGCGAAGAAAGCAATACGCTGATTTATCCCGCAATTTGCGCAATCGGACGCTG 900
 DB CTGTGCGAAGAAAGCAATACGCTGATTTATCCCGCAATTTGCGCAATCGGACGCTG 94771
 901 ATTTCGCGGCGGATGAATTTATGACAGAGCAAAAGCGCAATTA 948
 DB ATTTCGCGGCGGATGAATTTATGACAGAGCAAAAGCGCAATTA 94723

RESULT 23
 AAF21609/C
 ID AAF21609 standard; DNA; 349980 BP.
 XX

AC AAF21609;
 XX 13-MAR-2001 (first entry)
 DT Neisseria meningitidis B nucleotide sequence SEQ ID NO:110.
 XX Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;
 DE Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;
 KW diagnosis; antigen; detection; infection; gene therapy; antibacterial;
 KM ds.
 OS Neisseria meningitidis.
 XX MO20006791-AL.
 PN 09-NOV-2000.
 XX 08-MAR-2000; 2000WO-US005928.
 PF 30-APR-1999; 99US-013206BP.
 PR 08-OCT-1999; 99WO-US023573.
 PR 28-FEB-2000; 2000GB-00004695.
 XX (CHIR) CHIRON CORP.
 PA (GENO-) INST GENOMIC RES.
 XX P1 Pizza M, Hickey B, Peterson J, Tettelin H, Venter JC;
 PI Massignani V, Galeotti C, Mora M, Ratti G, Scarelli M, Scarlato V;
 PI Rappelli R, Frazer CM, Grandi G;
 DR WPI; 2000-647603/62.
 XX Neisseria meningitidis B full length genome sequence and open reading
 PT frames are used to detect, treat and prevent Neisserial infections.
 PS Claim 7; Appendix A; 692pp; English.
 XX The present invention describes the full length genome of Neisseria
 CC meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613
 CC represent fragments of the NMB genomic sequence, as the sequence was too
 CC long to go in a record on its own it was split into 8 sequences which
 CC overlap each other at the beginning and end of each sequence by 49980 bp
 CC (i.e. the last 49980 bp of AAF21544 is repeated at the beginning of
 CC AAF21607, the last 49980 bp of AAF21607 are repeated at the beginning of
 CC AAF21609, and so on). AAF21545 to AAF21588 encode the Neisseria proteins
 CC given in AAB58550 to AAB58593, and AAF21589 to AAF21606 represent PCR
 CC primers which are used in the exemplification of the present invention.
 CC The NMB genome and fragments from it have antibacterial activity, and can
 CC be used in vaccines and gene therapy. Neisseria nucleic acids, proteins
 CC and/or antibodies which binds to the proteins can be used in compositions
 CC for treating or preventing infection due to Neisserial bacteria or as a
 CC diagnostic reagent for detecting the presence of Neisserial bacteria or
 CC of antibodies raised to Neisserial bacteria. Computers, computer memory,
 CC computer storage medium or computer databases can be used in a search to
 CC identify open reading frames (ORFs) or coding sequences within the NMB
 CC genome. The DNA sequences provide further opportunities to find antigenic
 CC or immunogenic proteins which are more effective in vaccines than the
 CC outer membrane proteins currently used
 XX

Sequence 349980 BP; 81351 A; 86755 C; 95584 G; 86290 T; 0 U; 0 Other;
 SQ

Query Match 92.6%; Score 877.6; DB 3; Length 349980;
 Best Local Similarity 95.4%; Pred. No. 1.5e-253;
 Matches 904; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

1 ATGGAATTTTATTTATCTTTGTCAGCGCGCTTTGGCTTCAATCTTTGTC 60
 DB ATGGAATTTTATTTATCTTTGTCAGCGCGCTTTGGCTTCAATCTTTGTC 325222
 61 GTCAATCCCCAGAGAGTCCAGCTTTCGAAAGGCTGGGCGTTTCATCGCCCTG 120
 DB GTCAATCCCCAGAGAGTCCAGCTTTCGAAAGGCTGGGCGTTTCATCGCCCTG 325162
 121 AGGCGCGGTTTGAATTTTGAATTCCTTTATCGACCGGCTCCATCCGCAATCGCTG 180


```
Db 325161 ACGGCGGTTGAATATTTGATTCCTTTATCGACCGCGTCGCTACCGCATTCGCTG 325102
Qy 181 AAAAATATCCCTTTAGAGTACCCGACGAGTCTGATACAGCGGAGTAATACGAATTG 240
Db 325101 AAAAATATCCCTTTAGAGTACCCGACGAGTCTGATACAGCGGAGTAATACGAATTG 325042
Qy 241 ACTGTGACGGCATCATCTATTTCCAGTAACCGATCCCAATCTGCGCTCATACGGTTG 300
Db 325041 ACTGTGACGGCATCATCTATTTCCAGTAACCGATCCCAATCTGCGCTCATACGGTTG 324982
Qy 301 AGCAATCATATTATGCAATTACCCAGCTTGCCCAACGACGCTGCTTCGTTATCGGG 360
Db 324981 AGCAATCATATTATGCAATTACCCAGCTTGCCCAACGACGCTGCTTCGTTATCGGG 324922
Qy 361 CGTATGAGTTGAGCAAAACGTTTGAAGACGCGACGAAATCAACAGTACGCTCTCC 420
Db 324921 CGTATGAGTTGAGCAAAACGTTTGAAGACGCGACGAAATCAACAGTACGCTCTCC 324862
Qy 421 GCCCTCGATGAAAGCGCGGGGCTTGGGGTGTGAAGTCTCCGTTACGAAATCAAGGAT 480
Db 324861 GCTTTGACGAGGCGCGGGGCTTGGGGTGTGAAGTCTCCGTTACGAAATCAAGGAT 324802
Qy 481 TTGTTCCGCGCAAGAAATCTTTCGCGCAATGCAAGCAAAATTACCGCGCAACGCGAA 540
Db 324801 TTGTTCCGCGCAAGAAATCTTTCGCGCAATGCAAGCAAAATTACCGCGCAACGCGAA 324742
Qy 541 AAACGCGCGCGTATTCGCGCAATCCGAAGCGGTAAATTCGAACAATACCTTGCCAGT 600
Db 324741 AAACGCGCGCGTATTCGCGCAATCCGAAGCGGTAAATTCGAACAATACCTTGCCAGT 324682
Qy 601 GATCAGCGTGAAGCGCAATCCGAATCCGAAGCGGTAAATTCGAACAATACCTTGCCAGT 660
Db 324681 GATCAGCGTGAAGCGCAATCCGAATCCGAAGCGGTAAATTCGAACAATACCTTGCCAGT 324622
Qy 661 TCCAATGCGCAAGAAATGCGCGCATCAACGCGCGCAAGCGCAAGCGCAATCCCTGCGC 720
Db 324621 TCCAATGCGCAAGAAATGCGCGCATCAACGCGCGCAAGCGCAAGCGCAATCCCTGCGC 324562
Qy 721 CTTGTTCGCGCAAGCAATCCGCAAGCGCATTCGTCGAATTTGCGCGCGCTTCAAAACCAA 780
Db 324561 CTTGTTCGCGCAAGCAATCCGCAAGCGCATTCGTCGAATTTGCGCGCGCTTCAAAACCAA 324502
Qy 781 GCGCGGCGGAGTGGCGTCAATCTGAAGATGCGGAACATAGTAGCGCGCTTCAACAT 840
Db 324501 GCGCGGCGGAGTGGCGTCAATCTGAAGATGCGGAACATAGTAGCGCGCTTCAACAT 324442
Qy 841 CTTGCGCAAGAAAGCAATAGCGTGAATTTGCGCGCAATGTTGCGGATCGGACGCTG 900
Db 324441 CTTGCGCAAGAAAGCAATAGCGTGAATTTGCGCGCAATGTTGCGGATCGGACGCTG 324382
Qy 901 ATTTCTGCGCGCAATGAATTAATGACAGCAGCAAAACCGCGCAATTA 948
Db 324381 ATTTCTGCGCGCAATGAATTAATGACAGCAGCAAAACCGCGCAATTA 324334

RESULT 24
AAF21610/c
ID AAF21610 standard; DNA; 349980 BP.
XX
XX AAF21610;
XX
XX 13-MAR-2001 (first entry)
XX
XX Neisseria meningitidis B nucleotide sequence SEQ ID NO:111.
XX
XX Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;
XX diagnosis; antigen; detection; infection; gene therapy; antibacterial;
XX de.
XX Neisseria meningitidis.
XX
XX
XX WO200066791-A1.
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XX
PD 09-NOV-2000.
XX
PF 08-MAR-2000; 2000WO-US005928.
XX
PR 30-APR-1999; 99US-0132068P.
XX
PR 08-OCT-1999; 99WO-US023573.
XX
PR 28-FEB-2000; 2000GB-00004695.
XX
PA (CHIR ) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX
PI Pizza M, Hickey E, Peterson J, Tettelin H, Venter JC,
PI Maignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V,
PI Rappuoli R, Frazer CM, Grandi G,
XX
DR WPI; 2000-647603/62.
XX
PT Neisseria meningitidis B full length genome sequence and open reading
PT frames are used to detect, treat and prevent Neisserial infections.
XX
PS Claim 7; Appendix A; 692pp; English.
XX
CC The present invention describes the full length genome of Neisseria
CC meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613
CC represent fragments of the NMB genomic sequence, as the sequence was too
CC long to go in a record on its own it was split into 8 sequences which
CC overlap each other at the beginning and end of each sequence by 49980 bp
CC (i.e. the last 49980 bp of AAF21544 is repeated at the beginning of
CC AAF21607, the last 49980 bp of AAF21607 are repeated at the beginning of
CC AAF21608, and so on). AAF21545 to AAF21588 encode the Neisseria proteins
CC given in AAB58550 to AAB58593, and AAF21589 to AAF21606 represent PCR
CC primers which are used in the exemplification of the present invention.
CC The NMB genome and fragments from it have antibacterial activity, and can
CC be used in vaccines and gene therapy. Neisseria nucleic acids, proteins
CC and/or antibodies which binds to the proteins can be used in compositions
CC for treating or preventing infection due to Neisserial bacteria or as a
CC diagnostic reagent for detecting the presence of Neisserial bacteria or
CC of antibodies raised to Neisserial bacteria. Computers, computer memory,
CC computer storage medium or computer databases can be used in a search to
CC identify open reading frames (ORFs) or coding sequences within the NMB
CC genome. The DNA sequences provide further opportunities to find antigenic
CC or immunogenic proteins which are more effective in vaccines than the
CC outer membrane proteins currently used
XX
SQ Sequence 349980 BP; 86771 A; 92803 C; 86340 G; 8406 T; 0 U; 0 Other;
Query Match 92.6%; Score 877.6; DB 3; Length 349980;
Best Local Similarity 95.4%; Pred. No. 1.5e-253;
Matches 904; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
Qy 1 ATGGAATTTTTCATATCTGTTGGCAGCGTGGCGGTTTTCGGCTCAAAATCCTTTGTC 60
Db 25281 ATGGAATTTTTCATATCTGTTGGTGTAGCGTGGCGGTTTTCGGTTCAAAATCCTTTGTT 25222
Qy 61 GTCATCCCGCAGAGAGTCCAGTGTGCAAAAGCTCGGGCGCTTTCATCGCGCCCTG 120
Db 25221 GTCATCCCGCAGAGAGTCCAGTGTGCAAAAGCTCGGGCGCTTTCATCGCGCCCTG 25162
Qy 121 ACGGCGGTTGAAATATTTTGAATTCCTTTATGACGCGGCTGCGCTTACCGCATTCGCTG 180
Db 25161 ACGGCGGTTGAAATATTTTGAATTCCTTTATGACGCGGCTGCGCTTACCGCATTCGCTG 25102
Qy 181 AAAAATATCCCTTTAGAGTACCCGACGAGTCTGATACAGCGGAGTAATACGAATTG 240
Db 25101 AAAAATATCCCTTTAGAGTACCCGACGAGTCTGATACAGCGGAGTAATACGAATTG 25042
Qy 241 ACTGTGACGGCATCATCTATTTCCAGTAACCGATCCCAATCTGCGCTCATACGGTTG 300
Db 25041 ACTGTGACGGCATCATCTATTTCCAGTAACCGATCCCAATCTGCGCTCATACGGTTG 24982
Qy 301 AGCAATCATATTATGCAATTACCCAGCTTGCCCAACGACGCTGCTTCGTTATCGGG 360
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Db 24981 AGCAACTACATTATGAGCATTTACCGAGCTTGCCAAACGACGCTGCTTCCGTTATCGGG 24922
Qy 361 CGTATGAGTTGGACAAAACGTTTGAAGAACCGGACGAATCAACATACCTGCTTCC 420
Db 24921 CGTATGAGTTGGACAAAACGTTTGAAGAACCGGACGAATCAACATACCTGTTTGGG 24862
Qy 421 GCCCTCGATGAAAGCCGCGGGGCTTGGGGTGTGAAGTCTCCGTTACCAATCAAGAT 480
Db 24861 GCTTTGACAGAGCGCGCGGGCTTGGGGTGTGAAGTCTCCGTTATGAGTTTAAAGAC 24802
Qy 481 TTGTTCCGCGCCGCAAAATCCTTCGCGCAATGACGCAAAATTAACGCCGCAAGCGAA 540
Db 24801 TTGTTCCGCGCCGCAAAATCCTTCGCGCAATGACGCGCAAAATTAACGCCGCAAGCGAA 24742
Qy 541 AAACGCGCCGCTATTTGCGCAATCCGAAAGCGCGCTTAAATGAAACAATCAACTTGCAGT 600
Db 24741 AAACGCGCCGCTATTTGCGCAATCCGAAAGCGCGCTTAAATGAAACAATCAACTTGCAGT 24682
Qy 601 GGTTCAGCGTGAAGCCGCAAAATCCAAAGATCCGAAAGCGGAGCTCAGGCTGCGTCAATGCG 660
Db 24681 GGTTCAGCGTGAAGCCGCAAAATCCAAAGATCCGAAAGCGGAGCTCAGGCTGCGTCAATGCG 24622
Qy 661 TCCATGCGCGAAGAAATCGCGCGCATCAACCGCGCAAGCGGAAAGCGGAATCCTTGCGC 720
Db 24621 TCCATGCGCGAAGAAATCGCGCGCATCAACCGCGCAAGCGGAAAGCGGAATCCTTGCGC 24562
Qy 721 CTTGTTGCCGAAGCCCAATCGCGCAATCGGTCAAATTTGCGCGCCCTTCAAAACCA 780
Db 24561 CTTGTTGCCGAAGCCCAATCGCGCAATCGGTCAAATTTGCGCGCCCTTCAAAACCA 24502
Qy 781 GCGCGGCGCGATCGGTCATCTGAAGATTTGGGGAACATATGACCGCGCTTCAACAT 840
Db 24501 GCGCGGCGCGATCGGTCATCTGAAGATTTGGGGAACATATGACCGCGCTTCAACAT 24442
Qy 841 CTTGCAAAAGAAAGCAATACGCTGATTTATGCCCGCAATGTTGCCGACATCGGACGCTG 900
Db 24441 CTTGCAAAAGAAAGCAATACGCTGATTTATGCCCGCAATGTTGCCGACATCGGACGCTG 24382
Qy 901 ATTTCGCGCGATGAAATTTATCGACAGACCAAAACCGCAATTA 948
Db 24381 ATTTCGCGCGATGAAATTTATCGACAGACCAAAACCGCAATTA 24334

RESULT 25
AAZ53749
ID AAZ53749 standard; DNA; 850 BP.
XX
AC AAZ53749;
DT 15-SEP-2003 (revised)
DT 21-MAR-2000 (first entry)
XX
DE Neisseria gonorrhoeae ORF 519 partial DNA sequence SEQ ID NO:1447.
XX
KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
KW antibacterial; gene therapy; de.
OS Neisseria gonorrhoeae.
XX
PN WO9957280-A2.
XX
PD 11-NOV-1999.
XX
PF 30-APR-1999; 99WO-US009346.
XX
PR 01-MAY-1998; 98US-0083758P.
PR 31-JUL-1998; 98US-0094869P.
PR 02-SEP-1998; 98US-0098994P.
PR 02-SEP-1998; 98US-0099062P.
PR 09-OCT-1998; 98US-0103749P.
PR 09-OCT-1998; 98US-0103794P.
PR 09-OCT-1998; 98US-0103796P.
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PR 25-FEB-1999; 99US-0121528P.
XX
PA (CHIR ) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX
PI Fraser C, Galeotti C, Grandi G, Hickey E, Massignani V, Mora M;
PI Petersen J, Pizza M, Rappuoli R, Rateli G, Scalato E, Scarselli M;
PI Tettelin H, Venter JC;
XX
DR WPI, 2000-062150/05.
DR P-PSDB; AA74987.
XX
PT Novel Neisserial polypeptides predicted to be useful antigens for
PT vaccines and diagnostics.
XX
PS Claim 7; Page 776; 1453pp; English.
XX
CC AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941
CC represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides
CC and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55473 represent
CC PCR primers used in the exemplification of the present invention. The
CC polypeptides, the polynucleotides, antibodies and compositions of the
CC invention can be used as vaccines, as diagnostic reagents, and as
CC immunogenic compositions. The polypeptides can be used in the manufacture
CC of medicaments for treating or preventing infection due to Neisserial
CC bacteria (e.g. meningitis and septicemia), to detect the presence of
CC Neisseria bacteria, or to raise antibodies. They may also be used to
CC screen for agonists or antagonists, which may themselves have use as
CC antibacterial agents. The polynucleotides of the invention may also be
CC used in gene therapy protocols. (Updated on 15-SEP-2003 to standardise OS
CC field)
XX
SQ Sequence 850 BP; 215 A; 250 C; 205 G; 180 T; 0 U; 0 Other;

Query Match 88.6%; Score 840.4; DB 3; Length 850;
Best Local Similarity 99.3%; Pred. No. 1.7e-243;
Matches 844; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGGAATTTTTCATTTCTTGTGGACGCGTCCGCTTTTCCGCTTCAATCCTTTGTC 60
Db 1 ATGGAATTTTTCATTTCTTGTGGACGCGTCCGCTTTTCCGCTTCAATCCTTTGTC 60
Qy 61 GTTCATCCCGCAGAGAGTCCAGGTGTCGAAAGGCTCGGGCGTTTCATCGCGCCCTG 120
Db 61 GTTCATCCCGCAGAGAGTCCAGGTGTCGAAAGGCTCGGGCGTTTCATCGCGCCCTG 120
Qy 121 ACGGCGGTTTGAATTTTGAATTCCTTTATCGACCGCGTCCCTACCGCATTCGCTG 180
Db 121 ACGGCGGTTTGAATTTTGAATTCCTTTATCGACCGCGTCCCTACCGCATTCGCTG 180
Qy 181 AAAGAAATCCCTTTAGACGTACCCAGCGAGTTCGATCAGCGCGGATTAATTCGCAATTG 240
Db 181 AAAGAAATCCCTTTAGACGTACCCAGCGAGTTCGATCAGCGCGGATTAATTCGCAATTG 240
Qy 241 ACTGTTGACGCGATATCTATTTCCAAATACCAATCCCAATCTGCTCATACGCTTTC 300
Db 241 ACTGTTGACGCGATATCTATTTCCAAATACCAATCCCAATCTGCTCATACGCTTTC 300
Qy 301 AGCAACTACATTATGAGCAATTACCGAGCTTGCCCAACGACGCTGCTTCCGTTACGGG 360
Db 301 AGCAACTACATTATGAGCAATTACCGAGCTTGCCCAACGACGCTGCTTCCGTTACGGG 360
Qy 361 CGTATGAGTTGGACAAAACGTTTGAAGAACCGGACGAATCAACATACCTGCTTCC 420
Db 361 CGTATGAGTTGGACAAAACGTTTGAAGAACCGGACGAATCAACATACCTGCTTCC 420
Qy 421 GCCCTCGATGAAAGCCGCGGGGCTTGGGGTGTGAAGTCTCCGTTACCAATCAAGAT 480
Db 421 GCCCTCGATGAAAGCCGCGGGGCTTGGGGTGTGAAGTCTCCGTTACCAATCAAGAT 480
Qy 481 TTGTTCCGCGCCGCAAAATCCTTCGCGCAATGACGCGCAAAATTAACGCCGCAAGCGAA 540
Db 481 TTGTTCCGCGCCGCAAAATCCTTCGCGCAATGACGCGCAAAATTAACGCCGCAAGCGAA 540
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Qy 541 AAAGCGCCGCTATTGCGGAATCCGAAGGCGGTAAATCGAAACAATCAACTTGGCCAGT 600
Db 541 AAAGCGCCGCTATTGCGGAATCCGAAGGCGGTAAATCGAAACAATCAACTTGGCCAGT 600
Qy 601 GGTGAGCGGTGAAGCGGAATCCGAATCCGAAGGCGGTGAGTGGCGGTCAATGCG 660
Db 601 GGTGAGCGGTGAAGCGGAATCCGAATCCGAAGGCGGTGAGTGGCGGTCAATGCG 660
Qy 661 TCCGATGCGGGAATTCGCGCGCATCAACGCGCGCAAGGCGGAAGCGGATCCCTGGC 720
Db 661 TCCGATGCGGGAATTCGCGCGCATCAACGCGCGCAAGGCGGAAGCGGATCCCTGGC 720
Qy 721 CTGTGCGCGGAAGCAATGCGCGCAAGCCATCCGTCAATTCGCGCGCTTCAAAACCA 780
Db 721 CTGTGCGCGGAAGCAATGCGCGCAAGCCATCCGTCAATTCGCGCGCTTCAAAACCA 780
Qy 781 GCGCGGCGGATGCGGTCAATCTGAAGATTGCGGAACAATACGTAGCGCGGTCAACAT 840
Db 781 AGCGGCGGATGCGGTCAATCTGAAGATTGCGGACATACGTACCGGCTCAAAAT 840
Qy 841 CTGCGCAAG 850
Db 841 CTGCGCAAG 850

RESULT 26

AAZ54580
ID AAZ54580 standard; DNA; 600 BP.

AAZ54580;

21-MAR-2000 (first entry)

Neisseria meningitidis ORF 519 partial DNA sequence SEQ ID NO:3045.

Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
antibacterial; gene therapy; ds.

Neisseria meningitidis.

MO957280-A2.

11-NOV-1999.

30-APR-1999; 99WO-US009346.

01-MAY-1998; 98US-0083758P.
31-JUL-1998; 98US-0094869P.
02-SEP-1998; 98US-0098994P.
02-SEP-1998; 98US-0099062P.
09-OCT-1998; 98US-0103749P.
09-OCT-1998; 98US-0103794P.
09-OCT-1998; 98US-0103796P.
25-FEB-1999; 99US-0121528P.

(CHIR) CHIRON CORP.
(GENO-) INST GENOMIC RES.

Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;
Petersen J, Pizzo M, Rappuoli R, Ratti G, Scalato E, Scarselli M;
Teteljn H, Venter JC;

WPI; 2000-062150/05.
P-PSDB; AAY75778.

Novel Neisserial polypeptides predicted to be useful antigens for
vaccines and diagnostics.

Example 1; Page 73-74; 1453pp; English.

AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941

represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides
CC and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55473 represent
CC PCR primers used in the exemplification of the present invention. The
CC polypeptides, the polynucleotides, antibodies and compositions of the
CC invention can be used as vaccines, as diagnostic reagents, and as
CC immunogenic compositions. The polypeptides can be used in the manufacture
CC of medicaments for treating or preventing infection due to Neisserial
CC bacteria (e.g. meningitis and septicemia), to detect the presence of
CC Neisseria bacteria, or to raise antibodies. They may also be used to
CC screen for agonists or antagonists, which may themselves have use as
CC antibacterial agents. The polynucleotides of the invention may also be
CC used in gene therapy protocols

Sequence 600 BP; 166 A; 158 C; 159 G; 117 T; 0 U; 0 Other;

Query Match 57.7%; Score 547.2; DB 3; Length 600;

Best Local Similarity 94.5%; Pred. No. 7.9e-155;

Matches 567; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 349 TCCGTTATCCGGGCTATGAGTTGAGCAAAACGTTGAGAGACGAGCAAAATCAACAGT 408
Db 1 TCCGTTATCCGGGCTATGAGTTGAGCAAAACGTTGAGAGACGAGCAAAATCAACAGT 60

Qy 409 ACCGTGCTTCGCGCTTCGATGAAAGCCGCGGCGCTTGGGGTGAAGTCTCCCTTAC 468
Db 61 ACTGTGTGCGGCTTTGAGAGAGCGCGCGGCTTGGGGTGAAGTCTCCCTTAT 120

Qy 469 GAAATCAAGATTGTTCCGCGCGAGAAATCTTCGCGCAATGACGAGCAAAATTAAC 528
Db 121 GAGATTAAAGCTTGTTCCGCGCGAGAAATCTTCGCTCAATGACGCGCAAAATTAAC 180

Qy 529 GCGGACGCGGAAACGCGCGCGGCTATTGCGGAATCCGAAGCGCGTAATCGAACAAATC 588
Db 181 GCGGACGCGGAAACGCGCGCGGCTATTGCGGAATCCGAAGCGCGTAATCGAACAAATC 240

Qy 589 AACCTTGCAGTGTGAGCGTGAAGCGGAAATCCAAATCCGAAGCGGAGCTCAAGCT 648
Db 241 AACCTTGCAGTGTGAGCGGAGCGGAAATCCAAATCCGAAGCGGAGCTCAAGCT 300

Qy 649 GCGGTCAATGATGATGCGGAAATGCGCGCGCATCAACGCGCGCAAGGCGAAGCG 708
Db 301 GCGGTCAATGATGATGCGGAAATGCGCGCGCATCAACGCGCGCAAGGCGAAGCG 360

Qy 709 GAATCCCTGCGCTTGTGTCGAGAGCCGATGCGGCAATCCGCTCAATTCGCGCGCC 768
Db 361 GAATCCCTGCGCTTGTGTCGAGAGCCGATGCGGCAATCCGCTCAATTCGCGCGCC 420

Qy 769 CTTCAAAACCGAAGCGGCGGATGCGGTCAATCTGAAGATTGCGGAACAATACGTAGCC 828
Db 421 CTTCAAAACCGAAGCGGCGGATGCGGTCAATCTGAAGATTGCGGAACAATACGTAGCC 480

Qy 829 GCGTTCAACATCTTGCGCAAGAAAGCAATACGCTGATTTGCGCGCAATGTTGCGGAC 888
Db 481 GCGTTCAACATCTTGCGCAAGAAAGCAATACGCTGATTTGCGCGCAATGTTGCGGAC 540

Qy 889 ATCGGACGCGTATTTGCGCGCATGAAATTAATCGACGAGCAAAACCGCCAAATTA 948
Db 541 ATCGGACGCGTATTTGCGCGCATGAAATTAATCGACGAGCAAAACCGCCAAATTA 600

RESULT 27

AAAB1263
ID AAAB1263 standard; DNA; 600 BP.

AAAB1263;

04-DEC-2000 (first entry)

N. meningitidis partial DNA sequence m519. seq SEQ ID NO:968.

Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;
antigen; vaccine; diagnosis; infection; antibacterial; identification;
Meningococcus B; Memb; ds.

(i.e. the last 49980 bp of AAP21544 is repeated at the beginning of AAP21607, the last 49980 bp of AAP21607 are repeated at the beginning of AAP21608, and so on). AAP21545 to AAP21588 encode the Neisseria proteins given in AAB5550 to AAB58593, and AAP21589 to AAP21606 represent PCR primers which are used in the exemplification of the present invention. The NMB genome and fragments from it have antibacterial activity, and can be used in vaccines and gene therapy. Neisseria nucleic acids, proteins and/or antibodies which binds to the proteins can be used in compositions for treating or preventing infection due to Neisserial bacteria or as a diagnostic reagent for detecting the presence of Neisserial bacteria or of antibodies raised to Neisserial bacteria. Computers, computer memory, computer storage medium or computer databases can be used in a search to identify open reading frames (ORFs) or coding sequences within the NMB genome. The DNA sequences provide further opportunities to find antigenic or immunogenic proteins which are more effective in vaccines than the outer membrane proteins currently used

Sequence 600 BP; 166 A; 158 C; 159 G; 117 T; 0 U; 0 Other;

Query Match 57.7%; Score 547.2; DB 3; Length 600;

Best Local Similarity 94.5%; Pred. No. 7.9e-155;

Matches 567; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

```
Oy 349 TCCGTTATCGGCGGTATGAGTGGACAAACGTTTGAAGAACGGACGAATCAACAGT 408
Db 1 TCCGTTATCGGCGGTATGAGTGGACAAACGTTTGAAGAACGGACGAATCAACAGT 60
Oy 409 ACCGTCGTCCTCGCCCTCGATGAAAGCCCGCGGCGTTGGGGTGTAAAGTCTCCGTTAC 468
Db 61 ACTGTTGTTGGCGCTTGTGACAGAGCGCGCGGCGCTTGGGGTGTAAAGTCTCCGTTAT 120
Oy 469 GAAATCAAGATTGTTGTTCCGCGCGCAAGAAATCTTCGCGCAATGACGACCAATTAAC 528
Db 121 GAGATTAAAGACTTGTGTTCCGCGCAAGAAATCTTCGCTCAATGACGACCAATTAAC 180
Oy 529 GCCGAAACGCAAAAAACGCGCCGTTATGCGCAATCGAAGCGCGTAAATCGAACAAATC 588
Db 181 GCCGAAACGCAAAAAACGCGCCGTTATGCGCAATCGAAGCGCGTAAATCGAACAAATC 240
Oy 589 AACCTTGCCATGTGTGACGCGTGAAGCCGAATCCCAACATCCGAAGGAGGCTCAAGCT 648
Db 241 AACCTTGCCATGTGTGACGCGGCAAGCCGAATCCCAACATCCGAAGGAGGCTCAAGCT 300
Oy 649 GCGGTCATGCGTCCCAATGCGGCAAGAAATCGCGCGCATCAACCGCGCAAAAGCGAAGCG 708
Db 301 GCGGTCATGCGTCCCAATGCGGCAAGAAATCGCGCGCATCAACCGCGCAAAAGGTAAGCG 360
Oy 709 GAATCCCTGCGCTTGTGTTGCGGAAGCCCAATGCGCAAGCGCATCCGTCAAATTCGCGCGC 768
Db 361 GAATCCCTGCGCTTGTGTTGCGGAAGCCCAATGCGCAAGCGCATCCGTCAAATTCGCGCGC 420
Oy 769 CTTCAACCCCAAGGGGGGGCGGATCGGTCATCTGAAGATTGGGGAACATAGTAGCC 828
Db 421 CTTCAACCCCAAGGGGGGGCGGATCGGTCATCTGAAGATTGGGGAACATAGTAGCC 480
Oy 829 GCGTTCAACAATCTTGGCAAGAAAGCAATACGCTGATTATGCGCGCAATGTTGCGGAC 888
Db 481 GCGTTCAACAATCTTGGCAAGAAAGCAATACGCTGATTATGCGCGCAATGTTGCGGAC 540
Oy 889 ATCGGCAACCTGATTCTGCGCGCATGAAATTTATCGACAGAGCAAAACCGCCAAATTA 948
Db 541 ATCGGCAACCTGATTCTGCGCGCATGAAATTTATCGACAGAGCAAAACCGCCAAATTA 600
```

RESULT 29

AAZ53750 ID AAZ53750 standard; DNA; 600 BP.

XX AAZ53750;

XX 21-MAR-2000 (first entry)

DE Neisseria meningitidis ORF 519 partial DNA sequence SEQ ID NO:1449.

XX Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW antigenic; diagnostic; immunogenic; infection; meningitis; septicemia;
KW antibacterial; gene therapy; ds.

OS Neisseria meningitidis.

PN WO957280-A2.

PD 11-NOV-1999.

PF 30-APR-1999; 99WO-US009346.

PR 01-MAY-1998; 98US-0083758P.

PR 31-JUL-1998; 98US-0094869P.

PR 02-SEP-1998; 98US-0098994P.

PR 02-SEP-1998; 98US-0099062P.

PR 09-OCT-1998; 98US-0103749P.

PR 09-OCT-1998; 98US-0103794P.

PR 25-FEB-1999; 99US-0121528P.

PA (CHIR) CHIRON CORP.

PA (GENO-) INST GENOMIC RES.

PI Fraser C, Galeotti C, Grandi G, Hickey E, Maignani V, Mora M;
PI Petersen J, Pizsa M, Rappuoli R, Ratti G, Scalato E, Scarselli M;
PI Tettelin H, Venter JC;

DR WPI; 2000-062150/05.

DR P-PSDB; AAY74988.

XX Novel Neisserial polypeptides predicted to be useful antigens for
PT vaccines and diagnostics.

PS Claim 7; Page 777; 1453P; English.

CC AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941
CC represent novel Neisseria meningitis and N. gonorrhoeae polynucleotides
CC and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55473 represent
CC PCR primers used in the exemplification of the present invention. The
CC polypeptides, the polynucleotides, antibodies and compositions of the
CC invention can be used as vaccines, as diagnostic reagents, and as
CC immunogenic compositions. The polypeptides can be used in the manufacture
CC of medicaments for treating or preventing infection due to Neisserial
CC bacteria (e.g. meningitis and septicemia), to detect the presence of
CC Neisseria bacteria, or to raise antibodies. They may also be used to
CC screen for agonists or antagonists, which may themselves have use as
CC antibacterial agents. The polynucleotides of the invention may also be
CC used in gene therapy protocols

XX Sequence 600 BP; 165 A; 158 C; 159 G; 118 T; 0 U; 0 Other;

Query Match 57.4%; Score 544; DB 3; Length 600;

Best Local Similarity 94.2%; Pred. No. 7.4e-154;

Matches 565; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

```
Oy 349 TCCGTTATCGGCGGTATGAGTGGACAAACGTTTGAAGAACGGACGAATCAACAGT 408
Db 1 TCCGTTATCGGCGGTATGAGTGGACAAACGTTTGAAGAACGGACGAATCAACAGT 60
Oy 409 ACCGTCGTCCTCGCCCTCGATGAAAGCCCGCGGCGTTGGGGTGTAAAGTCTCCGTTAC 468
Db 61 ACTGTTGTTGGCGCTTGTGACAGAGCGCGCGGCGCTTGGGGTGTAAAGTCTCCGTTAT 120
Oy 469 GAAATCAAGATTGTTGTTCCGCGCAAGAAATCTTCGCGCAATGACGACCAATTAAC 528
Db 121 GAGATTAAAGACTTGTGTTCCGCGCAAGAAATCTTCGCTCAATGACGAGCGCAATTAAC 180
Oy 529 GCCGAAACGCAAAAAACGCGCCGTTATGCGCAATCGAAGCGCGTAAATCGAACAAATC 588
Db 181 GCCGAAACGCAAAAAACGCGCCGTTATGCGCAATCGAAGCGCGTAAATCGAACAAATC 240
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OY 589 AACCTTGCCAGTGTGTCAGCGTGAAGCCGAAATTCACATCCGAAGCGGCTGAGGT 648
DB 241 AACCTTGCCAGTGTGTCAGCGGCGAGCCGAAATTCACATCCGAAGCGGCTGAGGT 300
OY 649 GGGGTCATGGGTCCAAATGCGGAAATTCGCGCGCATCAACCGGCGGAAAGCGAGG 708
DB 301 GGGGTCATGGGTCCAAATGCGGAAATTCGCGCGCATCAACCGGCGGAAAGGTGAAGG 360
OY 709 GAATCCCTGCGGCTTGTGTCGCGGCAATGCGGCAAGCCATCCGTCAAATTCGCGCGG 768
DB 361 GAATCCCTGCGGCTTGTGTCGCGGCAATGCGGCAAGCCATCCGTCAAATTCGCGCGG 420
OY 769 CTTCAAAACCCAGGCGGCGGCGGATGCGGTCAATTCGAATATTCGGAACAAATACGTAAC 828
DB 421 CTTCAAAACCCAGGCGGCGGCGGATGCGGTCAATTCGAATATTCGGAACAAATACGTAAC 480
OY 829 GCGTCACAAATCTTGGCCAAAGAAAGCAATACGCGATATGCGCGCAATGTCGCGAC 888
DB 481 GCGTCACAAATCTTGGCCAAAGAAAGCAATACGCGATATGCGCGCAATGTCGCGAC 540
OY 889 ATCGGCAAGCTGATTTCTGCGCGCATGAAATATTCAGACAGCAAAACCGCAATTA 948
DB 541 ATCGGCAAGCTGATTTCTGCGCGCATGAAATATTCAGACAGCAAAACCGCAATTA 600

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RESULT 30

AAA12730
ID AAA12730 standard; DNA; 1677 BP.

AAA12730;

25-JUL-2000 (first entry)

DNA encoding of a plant stomatin-like polypeptide.

Maize; stomatin-like polypeptide; transgenic plant; disease resistance;
plant pathogen defense system; plant pest; fungal pathogen; virus;
nematode; insect; stomatin; univalent cation permeability; ion transport;
transformation efficiency; cell cycle; cell proliferation; cell growth;
86.

XX Zea mays.

Key Location/Qualifiers
FH 161..1345
FT /tag= a
FT /product= "stomatin-like polypeptide"

PN WO200015817-A2.

PD 23-MAR-2000.

PF 15-SEP-1999; 99WO-US021384.

PR 17-SEP-1998; 98US-0100748P.

PA (PION-) PIONEER HI-BRED INT INC.

PI Gordon-Kamm WJ, Lowe KS, Nandipalli R, Simmons CR;

DR MPI; 2000-271453/23.

DR P-PSDB; AAY84663.

XX New isolated plant stomatin-like gene used for producing transgenic
PT plants with enhanced disease resistance and for manipulating ion
XX transport in transformed plants and plant cells.

XX Claim 20; Page 66-67; 68pp; English.

CC The present sequence encodes a maize stomatin-like polypeptide. The
CC polynucleotide is used to produce transgenic plants with enhanced disease
CC resistance through activation of the plant pathogen defense system. Plant
CC pests which can be controlled in this manner include fungal pathogens,

CC viruses, nematodes and insects. Stomatin is an integral membrane protein
CC which functions as a negative regulator of univalent cation permeability.
CC The stomatin-like polynucleotide can therefore be used to manipulate ion
CC transport in transformed plants and plant cells which can result in
CC blocked or reduced cell cycle arrest, and increased transformation
CC efficiency. It can also be used for enhancing plant culture methods,
CC modulating the cell cycle and cell proliferation, and positively and
CC negatively manipulating cell growth

SQ Sequence 1677 BP; 460 A; 441 C; 406 G; 370 T; 0 U; 0 Other;

Query Match 18.4%; Score 174; DB 3; Length 1677;

Best Local Similarity 52.4%; Pred. No. 1.1e-41;

Matches 433; Conservative 0; Mismatches 360; Indels 33; Gaps 1;

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OY 60 CGTCATCCCGCAGCAGGAATCCAGTGTGCAAAAGCTCGGCGCTTCATCGGCGCT 119
DB 337 CATAGTTCGCGAGAGAGAGCTTACGTTGTGAGAGATTCGGGAAGTATTCAGAACCT 396
OY 120 GACGCGCGGTTGAATATTTGATTCCTTTATGACCGCGTCCGCTACCGCATTCGCT 179
DB 397 CGGCTCGGTTCCACCTTCGATCCCGCGTCGACCGTATTCCTTACGTCACTCGCT 456
OY 180 GAAAGAAATCCCTTGAAGTACGACCCAGCGAGTCTGATCAACGCGCATATACCAAT 239
DB 457 CAGGAGAGAGACATCCCTATCCCTCACCAGAACGCAATCAACAGAACGTAACCAT 516
OY 240 GACTGTGACGCGCATCATCTATTTCCAGATTAACGATCCCAATCGCTCATACGTTTC 299
DB 517 ACAGATGACGCGCATCATCTATTTCCAGATTAACGATCCCAATCGCTCATACGTTTC 576
OY 300 GAGCAATCAATTAATGCAATTAACCAAGTTCGCGCAACGCGTCCGTTATCGG 359
DB 577 GGAGATCCCAATCTATGCTGCTCTCAACCTTGCAAAACCAATGAGAGTGAAGTCCG 636
OY 360 GGTATGAGTGAAGCAAAACGTTTGAAGAAAGCGACGCAATCAACATACGTCGCTTC 419
DB 637 GAAAGTATCACTTATGATTAAGATCTTTGAGAGAGATGATTAATGAGAAATTTGAG 696
OY 420 CGCCCTCGATGAAGCGCGCGGCTTGGGTTGAAAGTCTCCGTTACGAATCAAGGA 479
DB 697 TGCATCATGAGAGAGAGAGAGAGATTTGGGCTGAAATGATTCGCTATGATGACAGGA 756
OY 480 TTTGTTCCGCGCAAGAAATCTTTCGCGCATTCAGGCAATTAACGCGGAAGCGGA 539
DB 757 CATTAATCTCTCAGAGAGAGATTAAGGAGCTATGAGATGAGGCTGAGGCGAGAAAGGA 816
OY 540 AAAAGCGCGCGTATTCGGAATCCGAATCCGAAGCGGTAAATCGAACAATCAACTTCCAG 599
DB 817 AAAAGCGCGCTCAAAATCTTGAATCAGAGAGGAAAGAAAGATGCGCAGATCTTTGA 854
OY 600 TGGTCAGCTGAAGCGGAATCCCAATCCGAAGCGAGGCTCAGGCTGCGCTCAATGC 659
DB 855 -----AGGCGCAATCTTGAATCAGAGAGGAAAGAAAGATGCGCAGATCTTTGA 903
OY 660 GTCCAAATGCGGAAATATCGCGCATCAACGCGCGCAAGCGGAATCCCTGGG 719
DB 904 ATCTGAAGAGCTATTTGATCTAGCAAAACGCTGCAAGGCTGCGGCTGAAGCAATTC 963
OY 720 CCTTGTTCGGAAGCGCAATCCGAAGCGCATTCGTCAAATTTGCGCGCGCTTCAACCA 779
DB 964 TGCCAAGTAGAAGCTACTGCTCGTGAATGAGATTTGTTTCAAGTCATGACCACTGA 1023
OY 780 AGGCGGCGGATGCGGTCAATCTGAAGATTCGGAACAAATAGTACGCGCTTCAACA 839
DB 1024 AGGCAATGCAAGGCTGATAGCTGAATCTTGAAGCAATCAATGAGCAATTCCTCAA 1083
OY 840 TCTTGCAAGAAAGCAATAGCTGATTAATGCGCGCATATGTTGCC 885
DB 1084 TCTGCACAAAAGCAAAATACATAGCTTCTTCCAGGTGATAGTCC 1129

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RESULT 31

PR 12-AUG-1999; 99US-0148613P.
 PR 27-AUG-1999; 99DE-01040764.
 PR 27-AUG-1999; 99DE-01040765.
 PR 27-AUG-1999; 99DE-01040766.
 PR 31-AUG-1999; 99DE-01040832.
 PR 31-AUG-1999; 99DE-01041378.
 PR 31-AUG-1999; 99DE-01041379.
 PR 31-AUG-1999; 99DE-01041380.
 PR 31-AUG-1999; 99DE-01041394.
 PR 31-AUG-1999; 99DE-01041396.
 PR 03-SEP-1999; 99DE-01042076.
 PR 03-SEP-1999; 99DE-01042077.
 PR 03-SEP-1999; 99DE-01042079.
 PR 03-SEP-1999; 99DE-01042086.
 PR 03-SEP-1999; 99DE-01042087.
 PR 03-SEP-1999; 99DE-01042088.
 PR 03-SEP-1999; 99DE-01042095.
 PR 03-SEP-1999; 99DE-01042124.
 PR 03-SEP-1999; 99DE-01042129.
 PR 09-MAR-2000; 2000US-0187970P.

XX (BADI) BASF AG.

PI Pompeius M, Kroegeer B, Schroeder H, Zelder O, Habernauer G;

DR WPI; 2001-137957/14.
 DR P-PSDB; AAB79725.

PT Nucleic acids from Corynebacterium glutamicum encoding metabolic pathway
 PT proteins, useful for producing fine chemicals in microorganisms,
 PT including organic acids, nonproteinogenic amino acids, and purine and
 PT pyrimidine bases.

PS Claim 3; Page 422-424; 1737p; English.

CC AAF171207 encode the Corynebacterium glutamicum metabolic
 CC pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum MP
 CC nucleic acids are useful for the production of fine chemicals in
 CC microorganisms, including organic acids, nonproteinogenic amino acids,
 CC purine and pyrimidine bases, nucleosides, lipids, saturated
 CC and unsaturated fatty acids, diols, carbohydrates, aromatic compounds,
 CC vitamins, cofactors, polyketides and enzymes

XX Sequence 1419 BP; 397 A; 416 C; 353 G; 253 T; 0 U; 0 Other;

Query Match 18.1%; Score 172; DB 4; Length 1419;
 Best Local Similarity 51.7%; Pred. No. 4,1e-41;
 Matches 391; Conservative 0; Mismatches 365; Indels 0; Gaps 0;

QY 12 CATTATCTGTTGGAGCGCGTTCGCTTTCGCTTCAATCCTTGTGTCATCCCA 71
 DB 121 CATAGTTTTCGTCGCTTGTGCGCGTGTGTGATCAAGTCATAGCCCTGATCCCA 180
 QY 72 GCAGGAAGTCCAGCTGTTGCGAAAGCTGGGCGTTCATGCGCCCTGACGCGCGTTT 131
 DB 181 GGGTGAACCGCGCTCATTTGAACGCTTGTGATGATACCGGCAACCGTTTCAAGGCGCT 240
 QY 132 GAATATTTTGAATCCCTTATGACCGGCGTCCATACCGCATTTGGCTGAAGAAATCC 191
 DB 241 GACCTGCTGTTTCATTCGTGACCGAGTACCGCAAGATCGACACCCGTGAGCGCT 300
 QY 192 TTTAGACGTACCGACGAGTCTGATCAGCGCGCATATATGCAATTAAGTGTGACG 251
 DB 301 GGTCTCATTTCCACGCGAGGCGTATATACCAACAGACGCGTGGCATGATAT 360
 QY 252 CATCATTTATTTCCAGTACCGATCCAAATCGCTCATATGCGTTGAGCACTACAT 311
 DB 361 CGTGTGACCTTCCAAATCAAGACGAGCGCCCATCTACGCGCTGGAACAATACAT 420
 QY 312 TATGCAATTAACCGAGTGGCCAAAGACGCGTTCGTTATCGGCGATGAGATT 371
 DB 421 CGTGTGTGAGACGATTTCTGTAGCAACCTTGAGACGTTGCGGTGATGACCT 480

QY 372 GCACAAACGTTTGAGAGACGACGAAATCAAGATACCGTGTCTCCGCCCTGATGA 431
 DB 481 GGAAGAAACCTTCACTTACGTGACGTATCAACCGCGCTCCGTGTGCGAGCTGATGC 540
 QY 432 AGCCGCCGGGCTTGGGTGTGAAAGTCTCTCGTTAGCAATTCAGATTTGTTGCC 491
 DB 541 AGCAACCAACAAATGGGGCTGCGCATGAGCTGTGTGAACATAAGCAATTTGATCC 600
 QY 492 GCAAGAAATCTTCCGCGCATATGACAGGCAATTAACCGCAACGCAAAACGCGCCG 551
 DB 601 ACATTCATTCAGCATATGATGAGAAAGCAATGAGCAACCTGAAAACGCGCCAC 660
 QY 552 TATGCGCAATTCGAGGCGGTAAATTCGAAATCAATCACTTGTGCACTGTCAGCGTGA 611
 DB 661 CATTTTGACCCGAGAGGTACGCGGAAGCCGACATCAAACTGCCGGAAGTGAAGCA 720
 QY 612 AGCCGAATTCGAAATTCGGAAGCGGAGCTTCAGGCTCGGTCATATGTTGCCGA 671
 DB 721 AGCCAAAGTCTTCCAAAGCTGAGGTTGAAAGACGCGCATTCATCTTGAACGAGAA 780
 QY 672 GAAATCGCCCGCATCAACCGCGCAAAAGGCGAAGCGGAATCCCTGCGCTTGTGCCGA 731
 DB 781 AGCCCAAGCATGATCTCGCGCGCGGAGGAGTGAAGCGGACAGCATCTTCCAGGCGCA 840
 QY 732 AGCCAAATGCGAGGCGATCGCTCAATTTCCGCGCGC 767
 DB 841 GGTGTGAACCCGAGCAATCCAAAGGTCAACGCGAGC 876

RESULT 34

AAAF1207 standard; DNA; 1419 BP.

XX AAF1207;

DT 30-APR-2001 (first entry)

DE Corynebacterium glutamicum HA protein nucleotide sequence SEQ ID NO:139.

KM Corynebacterium glutamicum; homeostasis; adaptation; HA protein;
 KM fine chemical production; organic acid; proteinogenic amino acid;
 KM nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside;
 KM nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;
 KM carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme;
 KM diagnosis; Corynebacterium diphtheriae; genetic engineering;
 KM Brevibacterium; environmental condition; de.

OS Corynebacterium glutamicum.

PN WO200100842-A2.

PD 04-JAN-2001.

PF 23-JUN-2000; 2000WO-IB000911.

XX 25-JUN-1999; 99US-0141031P.
 XX 08-JUL-1999; 99DE-01031636.
 XX 09-JUL-1999; 99DE-01032125.
 XX 09-JUL-1999; 99DE-01032126.
 XX 09-JUL-1999; 99DE-01032127.
 XX 09-JUL-1999; 99DE-01032128.
 XX 09-JUL-1999; 99DE-01032226.
 XX 09-JUL-1999; 99DE-01032230.
 XX 14-JUL-1999; 99DE-01032920.
 XX 14-JUL-1999; 99DE-01032922.
 XX 14-JUL-1999; 99DE-01032924.
 XX 14-JUL-1999; 99DE-01032928.
 XX 14-JUL-1999; 99DE-01032930.
 XX 14-JUL-1999; 99DE-01032933.
 XX 14-JUL-1999; 99DE-01032935.
 XX 14-JUL-1999; 99DE-01032973.
 XX 14-JUL-1999; 99DE-01033002.
 XX 14-JUL-1999; 99DE-01033003.

PR 14-JUL-1999; 99DE-01033005.
 PR 14-JUL-1999; 99DE-01033006.
 PR 31-AUG-1999; 99DE-01041378.
 PR 31-AUG-1999; 99DE-01041379.
 PR 31-AUG-1999; 99DE-01041390.
 PR 31-AUG-1999; 99DE-01041391.
 PR 03-SEP-1999; 99DE-01042088.
 PA (BADI) BASF AG.
 XX
 PI Pompejus M, Kroeger B, Schroeder H, Zelder O, Haberhauer G;
 DR WPI; 2001-061974/07.
 DR P-PSDB; AAB79092.
 XX
 PT New isolated Corynebacterium glutamicum nucleic acid for production or
 PT modulation of production of fine chemicals such as amino acids,
 PT nucleosides, nucleotides, lipids, fatty acids, carbohydrates, vitamins or
 PT enzymes.
 PS
 XX
 PS Claim 3; Page 340-342; 712pp; English.
 XX
 CC AAF71138 to AAF71357 encode the Corynebacterium glutamicum homeostasis
 CC and adaptation (HA) proteins given in AAB79092 to AAB79242. The C.
 CC glutamicum HA genes (I) can be used in vectors for expression in host
 CC cells and production of fine chemicals, such as, an organic acid,
 CC proteinogenic or nonproteinogenic amino acid (preferred), purine or
 CC pyrimidine base, nucleoside, nucleotide, lipid, saturated or unsaturated
 CC fatty acid, diol, carbohydrate, aromatic compound, vitamin, cofactor,
 CC polyketide or enzyme. The amino acids produced can be lysine, glutamine,
 CC glutamate, alanine, aspartate, glycine, serine, threonine, methionine,
 CC cysteine, valine, leucine, isoleucine, arginine, proline, histidine,
 CC tyrosine, phenylalanine, or tryptophan. The fine chemical production can
 CC be modulated. The presence of (I) or HA proteins encoded by then are used
 CC for diagnosing the presence or activity of Corynebacterium diphtheriae.
 CC (I) can be used to map the C. glutamicum genome or can be used as markers
 CC for genetically engineered Corynebacterium or Brevibacterium. The HA
 CC proteins encoded by the (I) are used to maintain homeostasis in C.
 CC glutamicum or help the microorganism to adapt to different environmental
 CC conditions
 CC
 XX
 SQ Sequence 1419 BP, 397 A, 416 C, 353 G, 253 T, 0 U; 0 Other;
 Query Match 18.1%; Score 172; DB 4; Length 1419;
 Best Local Similarity 51.7%; Pred. No. 4.1e-41;
 Matches 391; Conservative 0; Mismatches 365; Indels 0; Gaps 0;

DB 481 GGAGAAACCTCACTTCACGTGACGTGATCAACCGCCGCTCGTGGAGCTTCATGC 540
 QY 432 AGCCGCCGGGGCTTGGGGTGGAAAGTCTCGTTAGAAATCAAGATTTGTTCCGCC 491
 DB 541 AGCAACCAACCAATGGGGCTCGGCATGACCGTGTGAACTAAAGGCAATTTGATCCGCC 600
 QY 492 GCAAGAAATCTTGGCGCAATGACAGGCAAAATTAACCGCCGAAACGCAAAACGCGCCG 551
 DB 601 ACCATCCATCCAGCAATGATGAGAAACGATGAGCAAGACGCGTGAAGCGGCCAC 660
 QY 552 TATGCGCAATCCGAAGCCGCTAAATGAAACAAATCAACTTGGCACTGCTACGCTGA 611
 DB 661 CATTTTGAACCGAGAAAGTCAAGCCGGAAGCCGACATCAAACTGCGGAAAGTGAAGAGA 720
 QY 612 AGCCGAATCCAAATCCGAAGGAGGCTTCAGGCTCGGTCAATGGCTCAATGCCGA 671
 DB 721 AGCCGAATCTCTCCAACTGAGGGTGAAGAGCAATCCATTCATTCGAACGCAAGACAGA 780
 QY 672 GAAATTCGCGCATCAACCGCGCCAAAGGCGGAATTCCTGCGCTTGTTCGCGA 731
 DB 781 ACCCAAGCATGATCTCTGCGCGCCGGAAGTGAAGCCGACGACCTCAAGCGCGCA 840
 QY 732 AGCCGAATCCGAAGGCAATCCGTCAAATTTGCCGCGCGC 767
 DB 841 GGGTGAAGCCGAGCAATCCAAAGGTCAACGACGAC 876
 RESULT 35
 ADD13438
 ID ADD13438 standard; DNA; 1426 BP.
 AC ADD13438;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DB C. glutamicum metabolic pathway associated DNA RXA00152.
 XX
 KW db; gene; metabolic pathway regulation; fine chemical; lysine;
 KW nucleotide; nucleoside; lipid; fatty acid; diol; carbohydrate;
 KW aromatic compound; vitamin; co-factor; enzyme; food; animal feed;
 KW cosmetic; pharmaceutical.
 XX
 OS Corynebacterium glutamicum.
 XX
 FH Key Location/Qualifiers
 FT CDS 101..1399
 FT /*tag= a
 XX
 PN MO2003040681-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 31-OCT-2002; 2002MO-BP012141.
 XX
 PR 05-NOV-2001; 2001DE-01054292.
 XX
 PA (BADI) BASF AG.
 XX
 PI Zelder O, Pompejus M, Schroeder H, Kroeger B, Kloppegg G;
 PI Haberhauer G;
 XX
 DR WPI; 2003-482273/45.
 DR P-PSDB; ADD13439.
 XX
 PT New nucleic acid encoding variant forms of metabolic regulatory proteins,
 PT useful for production of fine chemicals, specifically lysine, in
 PT microorganisms.
 PS
 PS Claim 1; SEQ ID NO 5; 328pp; German.
 XX
 CC This invention describes novel Corynebacterium glutamicum
 CC polynucleotides, polypeptides and variants associated with the regulation
 CC of metabolic pathways. The products of the invention are used for

CC production of fine chemicals, preferably amino acids and specifically
CC lysine, but more generally nucleosides, nucleosides, lipids, fatty acids,
CC diols, carbohydrates, aromatic compounds, vitamins, co-factors and
CC enzymes, useful in the food, animal feed, cosmetics and pharmaceutical
CC industries. The polynucleotides of the invention, optionally as primers
CC and probes, can also be used for identification and classification of C.
CC glutamicum and related species, e.g. for diagnosis, for genomic mapping,
CC functional or evolutionary studies, gene manipulation and modulation of
CC metabolic activity. Cells containing the products of the invention may
CC produce fine chemicals in improved yields, with higher productivity
CC and/or more efficiently.

XX Sequence 1426 BP; 401 A; 418 C; 354 G; 253 T; 0 U; 0 Other;

XX Query Match 18.1%; Score 172; DB 10; Length 1426;

XX Best Local Similarity 51.7%; Pred. No. 4.1e-41;
Matches 391; Conservative 0; Mismatches 365; Indels 0; Gaps 0;

QY 12 CATTATCTTTGGTGGACGCGCTGCGGCTTTGCGCTTCAATCTTTGTGTCATCCCCCA 71
DB 121 CATAGTTTTCCTGCTTTGTCGCGCTGCTGCTGATCAAGTCATAGCCCTGATCCCCCA 180
QY 72 GCAGGAAGTCCACGTTGTGGAAGGCTGCGGCTTCCATCGCGCCCTGACGCGGCTT 131
DB 181 GGGTGAAGCGCGCTGCTGATTAAGCGCTTGTAGTACACCGCTTTCAGGTGGCT 240
QY 132 GAATATTTTGTATTCCTTTATGACGCGCTGCTTACGCGCATGCTGCTGAAGAATCCC 191
DB 241 GACCTGCTGCTGCTTCACTTGTGACCGAGTACGCGCAAGATGACACCCGCTGAGCGCT 300
QY 192 TTTAGACGTACCGACCGAGTGTGATCATCGCGCATTAATGCAATTGACTGTTGACGG 251
DB 301 GGTCTCATTTCCACGCGAGGCTGTTATTATCCAGAACCACTGACCGTGGCATGATAT 360
QY 252 CATCATCTATTTCCAGTACCGATCCCAAACTGCGCTCATGCGTGTGAGAACTATCAT 311
DB 361 CGTGTGACCTTCCAAATCAAGAACCGAGCGCGCATTAAGCGCTGAGAACTATCAT 420
QY 312 TATGCAATTTACCAAGTCTGCGCAACGACGCTGCTTCCGTTATCGGCGTATGAGTT 371
DB 421 CGTGTGTGTGAGCAGATTTCTGTAGCAACTTGTGAGACGTTTGTGCGGATGACCT 480
QY 372 GGAAGAAAGCTTTGAAAGACGCGCAATCAACAGTACCGTGTCTCGCCCTGATGA 431
DB 481 GGAAGAAAGCTTCACTTCAAGTGTATCAACGCGCGCTCGTGGAGAGCTGATGAC 540
QY 432 AGCGCGCGGCGCTGCGGTGTAAGTCTCGCTTACGAAATCAAGATTTGTTCCGCC 491
DB 541 AGCAACCAACCAATGCGCGCTGCGATCAGCGCTGTGAACTTGAAGGCAATTTGATCC 600
QY 492 GCAAGAAATCTTCTCGCGCATGACGACCAATTAACCGCGCAACCGCAAAACGCGCCG 551
DB 601 ACCATTCATCCAGCAATGATGAGAAAGATGAAAGGACGACCTGAAAGAGCGGCGAC 660
QY 552 TATTGCGCAATCCGAAGCGCTGAAATGCAACCAATCAACTTGTGCAAGTGTGACGCTGA 611
DB 661 CATTTGACCGGAGAGGTCAAGCGGAGGACGACATCAAACTGCGGAGGAGGAAAGCA 720
QY 612 AGCGCAATTCGAAGCTGGAAGGCGAGGCTGAGGCTCGGTCATGCGTCCATGCGCGA 671
DB 721 AGCGCAAGTCTTCAAGCTGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
QY 672 GAAATTCGCGCGCATCAACCGCGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 731
DB 781 AGCGCAAGGAGTATCTGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
QY 732 AGCGCAATCCGAAGCGCTGCAATTTGCGCGCGC 767
DB 841 GGGTGAAGCGCGGAGCAATCCAAAGTCAAGCGACG 876

RESULT 36
AAH68529/c

ID AAH68529 standard; DNA; 349980 BP.

XX AAH68529;

XX 26-SEP-2001 (first entry)

XX C glutamicum coding sequence fragment SEQ ID NO: 7064.

XX Corynebacterium; amino acid synthesis; vitamin; saccharide;

XX organic acid synthesis; ds.

XX Corynebacterium glutamicum.

XX EP1108790-A2.

XX 20-JUN-2001.

XX 18-DEC-2000; 2000EP-00127688.

XX 16-DEC-1999; 99JP-00377484.

XX 07-APR-2000; 2000JP-00159162.

XX 03-AUG-2000; 2000JP-00280988.

XX (KIOWA) KIOWA HAKKO KOGYO KK.

XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;

XX Tateishi N, Senoh A, Ikeda M, Ozaki A;

XX WPI, 2001-376931/40.

XX Novel polynucleotides derived from Corynebacterium bacteria, for identifying

XX mutation point of a gene, measuring expression of a gene, analyzing

XX expression profile or pattern of a gene and identifying homologous gene.

XX Disclosure; SEQ ID NO 7064; 246pp + Sequence Listing; English.

XX The present invention provides a number of nucleotide and protein

XX sequences from the Corynebacterium bacteria Corynebacterium glutamicum. These

XX are useful for identifying the mutation point of a gene derived from a

XX mutant of corynebacterium bacteria, measuring expression amount and analyzing

XX the expression profile or expression pattern of a gene derived from

XX Corynebacterium bacteria, and identifying a homologue of a gene derived from

XX corynebacterium bacteria. Corynebacterium bacteria are useful for producing amino

XX acids, nucleic acids, vitamins, saccharides and organic acids,

XX particularly L-lysine. The present sequence is a nucleic acid described

XX in the exemplification of the invention. Note: The sequence data for this

XX patent did not form part of the printed specification, but was obtained

XX in electronic format directly from the European Patent Office

XX Sequence 349980 BP; 82466 A; 95954 C; 90516 G; 81044 T; 0 U; 0 Other;

XX Query Match 18.1%; Score 172; DB 5; Length 349980;

XX Best Local Similarity 51.7%; Pred. No. 5.1e-40;

XX Matches 391; Conservative 0; Mismatches 365; Indels 0; Gaps 0;

QY 12 CATTATCTTTGGTGGACGCGCTGCGGCTTTGCGCTTCAATCTTTGTGTCATCCCCCA 71

DB 119596 CATAGTTTTCCTGCTTTGTCGCGCTGCTGCTGATCAAGTCCATAGCCCTGATCCCCCA 119537

QY 72 GCAGGAAGTCCACGTTGTGGAAGGCTGCGGCTTTCCATGCGCGCTGACGCGGCTT 131

DB 119536 GGGTGAAGCGCGCTGCTGATTAAGCGCTTGTAGTACACCGCGACCGCTTTCAGGTGGCT 119477

QY 132 GAATATTTTGTATTCCTTTATGACGCGGTGCGCTTACCGCATTCGCTGGAAGAATCCC 191

DB 119476 GACCTGCTGCTGCTTCACTTGTGAGCCAGATGACGAGATGCAACCCGCTGAGCGCT 119417

QY 192 TTTAGACGTACCGACGAGTGTGATCAGCGCGCATTAATGCAATTGACTGTTGACGG 251

DB 119416 GGTCTCATTTCCACGCGAGGCTGTTATTATCCAGAGCACTGACCGGCTGATGATAT 119357

QY 252 CATCATCTATTTCCAGTACCGATCCCAAACTGCGCTCATAGGTTGAGCAACTATCAT 311

Db 119356 CGTGTGACCTTCCAAATCAAGAACGAGCGCCCATCTAAGCGGTGAGCACTACAT 119297
 Qy 312 TATGGCAATTACCCAGCTTGCCCAACGACGCTGCGTTCCGTATCGGCGTATGAGTT 371
 Db 119296 CCGTGGGTGAGACGATTTCTGTAGCAACATTCGAGACGTTGTCGGTGCATGACCT 119237
 Qy 372 GGAAGAAAGCTTGAAGAACGAGCAAGAAATCAACAGTACCGTCTCGCCCTGATGA 431
 Db 119236 GGAAGAAAGCTTCACTTCACTGAGACGTATCAACCGCCCTCTCGTGGAGCTGATGC 119177
 Qy 432 AGCCCGCGGGGCTTGGGGTGTGAAGTCTCGCTTCAAGAAATCAAGATTTGGTCCGC 491
 Db 119176 AGCAACCAACCAATGAGGCGCTGCGCATCAGCCTGTGGAACCTAAGGCAATGATCCGC 119117
 Qy 492 GCAGAAATCTTTCGGCAATGACGACGCAAAATTAACCGCCGAACGCGAAACGCGCCG 551
 Db 119116 ACCATCATTCAGCAATCATGAGAAAGAGATGAAAGAGACGCGGAAAGCGCCAC 119057
 Qy 552 TATTCGCCAATCGAAGGCGCTTAAATTCGAACAAATCACTTCCAGTGTCAAGGTGA 611
 Db 119056 CATTTTGACCGAGAAAGTTCAGCGCGAAGCCGACATCAAACTCGAAGGTGAAGCA 118997
 Qy 612 AGCCGAATTCACCAATTCGAAAGCGAGGCTCAGCTGCGGTCAATGCTCCATGCCA 671
 Db 118996 AGCAAGATCTTCAAGCTGAGGTTGAAAGACGATCATCTGAAGCAGAGACGA 118937
 Qy 672 GAAATCGCCCGCATCAACCGCCCAAGCGGAAATCCCTGCGCTTGTGCGCA 731
 Db 118936 AGCCCAAGGATATCTCTGGCGCGCAAGGTGAACGCGAGCAGCTACTCCAGCGCA 118877
 Qy 732 AGCCAAATGCCGAAGCCATCCGTCAAAATTCGCGCGCG 767
 Db 118876 GGGTGAAGCCCGAGCAATCCAAAGGTCAACGAGC 118841

RESULT 37
 ABL05449
 ID ABL05449 standard; cDNA; 1153 BP.
 XX
 AC ABL05449;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 10829.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KM pharmaceutical; gene; ss.
 XX
 OS Drosophila melanogaster.
 XX
 PN W0200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001MO-US009231.
 XX
 PR 23-MAR-2000; 2000US-0191637P.
 XX
 PR 11-JUL-2000; 2000US-00614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI: 2001-656860/75.
 DR P-PSDB; ABB61346.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.
 XX
 PS Claim 1; SEQ ID NO 10829; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent

CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins (AB857737-
 CC AB872072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp://wipo.int/pub/published_pcr_sequences

XX Sequence 1153 BP; 298 A; 297 C; 333 G; 225 T; 0 U; 0 Other;

SQ Query Match 17.5%; Score 165.6; DB 4; Length 1153;

Best Local Similarity 51.8%; Pred. No. 3.2e-39;

Matches 427; Conservative 0; Mismatches 364; Indels 33; Gaps 1;

Qy 56 TTGTGTCATCCCGCAGAGAAAGTCAAGTTCGAAAGGCTCGGGGTTTCCATCCG 115
 Db 152 TTATGTTGTGCCCCAGCAAGAGCGCTGGGTGTGAGACGCAATGGGCGCTTTCACAGGA 211
 Qy 116 CCGTACGCGCGGTTGAAATATTGATTCCTTTATGACCGGTCGCTACCGCAT 175
 Db 212 TTTTGACCCCGACTCAACATATGATCCGCTGCGGACCAAAATCAATACGTCCAGA 271
 Qy 176 CGCTGAAGAAATCCCTTTAGACGTACCGACGAGCTGATCAACGCGCATTAATACGC 235
 Db 272 GCTTGAAGAAATTCGCTATGATGTGCCAAACAGAGCTATTAATCTCCGACAACTGTA 331
 Qy 236 AATTGACTGTGACGCGATCATCTATTTCAGATTAACGATCCAACTCGCTCATACG 295
 Db 332 CCGTAGATGACGCGCGGTCTCTACTTCCGATCATGATCCGTAACAAAGCTGTACG 391
 Qy 296 GTTCAGACAATCAATATGAGCAATTAACCACTTCCCAACGACGCTGCTCCGTTA 355
 Db 392 GCGTGAAGATCCGAGTTCGCGCATTAACAACATGCGCCAGACGAGATGAGTGGAGC 451
 Qy 356 TCGGGCGTATGAGTTGACAAAGCTTTGAAGACGACGAAATCAACAGTACCGTGC 415
 Db 452 TGGGCAAGATGTCATGACAGAGGTCTTCGGGAAAGAGATGCTTCAACGTACAGATCG 511
 Qy 416 TCTCGCCCTCGATGAGAGCGCGGCTTGGGGTGTGAAGTCTTCGTTACGAATCA 475
 Db 512 TCGACTCGATCAACAAGCGCAGCGAGGCGTGGGATCGCTGTGCGATACGAGATCG 571
 Qy 476 AGGATTTGTTCCGCGCAAGAAATCTTCGCGCAATGAGCAACAAATTAACCGCGAAC 535
 Db 572 GTGATATTGACTGCGCCACAGGTTTCAAGAGCGATGCAAGTGAAGGCCGAGC 631
 Qy 536 GCGAAAGAGCGCCGCTATTGCGGAATCCGAAGCGGTAAATTCGAACAAATCAACTTG 595
 Db 632 GCGAAAGAGCGCGCTATTCTGAAATCGGA----- 662
 Qy 596 CCAATGTCAGCGTGAAGCGCAATTCACAAATTCGGAAGCGAGGCTCAGGTCGCGTCA 655
 Db 663 -----GGGTGTTGGCGAGCGCGAATCAACATGCGGAGGCAAGCGAAGTCTAGGATTC 718
 Qy 656 ATGCGTCAATGCGGAAATTCGCCCGCATCAACCGCCCAAGCGCAAGCGGAATCCC 715
 Db 719 TAGCTTCGAGCGGAGCGCGAGACACATTAAGGCAAGCGGAGAGGCGGCTGCCA 778
 Qy 716 TCGCCTTGTGCGGAAGCAATGCGGAAGCCATCGCAATTAATGCGCGCGCTTCAAA 775
 Db 779 TTATAGCCGTGGGAGTGCAGAGCCGCAATCTAATGCGCATAGGAAATCTTATCCC 838
 Qy 776 CCCAAGCGCGGCGATGCGGTCAATCTGAAGATTGCGGACAAATACGTAGCGCGCTTCA 835
 Db 839 ACTGTGATGACAGATGTGCTGCTCAGCGTGCAGAGAGTACATGAGGCTTCA 898
 Qy 836 ACAATTTGCCAAGAAAGCAATAGCTGATTAATGCGCGCAAT 879
 Db 899 AGAAGCTGCCAAGAGCAATTAACCATGATCTTGCCCTTGAT 942

RESULT 38
ADJ39266 standard; cDNA; 1218 BP.
AC ADJ39266;
DT 06-MAY-2004 (first entry)
XX Plant cDNA #266.
XX
XX Plant; gene; ss; transcription; plant genome augmentation; cereal;
XX soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
XX maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
XX stress tolerance; salt tolerance; cold tolerance; drought tolerance;
XX plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
XX antifungal.
XX Eukaryota.
XX
XX US2004016025-A1.
XX
XX 22-JAN-2004.
XX
XX 26-SEP-2002; 2002US-00260238.
XX
XX 26-SEP-2001; 2001US-0325277P.
XX 26-SEP-2001; 2001US-0325448P.
XX 04-APR-2002; 2002US-0370620P.
XX
XX (BUDWORTH P.
XX (MOUGHAMER T.
XX (BRIGGS S P.
XX (COOPER B.
XX (GLAZER GLAZERBROOK J.
XX (GOLF S A.
XX (KATA KATAGIRI F.
XX (KREPS J.
XX (PROV PROVART N.
XX (RICK RICE D.
XX (ZHU ZHU T.
XX
XX Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J;
XX Golf SA, Katagiri F, Kreps J, Provart N, Riche D, Zhu T;
XX
XX WPI; 2004-190374/18.
XX
XX New rice promoter, useful for manipulating crop plants to alter or
XX improve phenotypic characteristics, e.g. produce large quantities of oil
XX or proteins, resistance to insecticides, virus or fungi, stress tolerance
XX or high nutritional value.
XX
XX Claim 68; SEQ ID NO 266; 230bp; English.
XX
XX The invention relates to plant nucleotide sequences that direct seed-,
XX leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential
XX or constitutive transcription of an operatively linked nucleic acid
XX segment. The invention also relates to a method for augmenting a plant
XX genome and a method of identifying a gene, where its expression is
XX altered in the seed, leaf, stem, panicle, pollen, root or is constitutive
XX in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
XX canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,
XX sorghum, rice or wheat. The polynucleotides and the polypeptides they
XX encode are useful for manipulating crop plants to alter or improve
XX phenotypic characteristics, to produce large quantities of oil or
XX proteins, to incur resistance to insecticides, viruses or fungi, and to
XX incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
XX have a high nutritional value with reduced apical dominance or dwarfism,
XX early flowering or altered metabolic pathways. This sequence represents a
XX plant nucleic acid of the invention. Note: The sequence data for this
XX patent did not form part of the printed specification but was obtained in
XX electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX Sequence 1218 BP; 289 A; 348 C; 329 G; 252 T; 0 U; 0 Other;

Query Match 16.9%; Score 160.2; DB 12; Length 1218;
Best Local Similarity 53.4%; Pred. No. 1.4e-37;
Matches 336; Conservative 0; Mismatches 293; Indels 0; Gaps 0;
QY 60 CGTCATCCCCCAGAGAGAGATCCAGTGTTCGAAAAGCTCGGCGTTCCATCGCGCCT 119
DB 258 CATCGTCGCGAGAGAGAGAGAGAGCGTTCGTGTGTGAGCGGTCGGAAGTCAAGAGCGCT 317
QY 120 GACGCGCGGTTTGAATTTTGAATTCCTTATATGACCGGTGCGCTTACCGGCT 179
DB 318 CGGCTCGGAGTTCACGCTGCTGCTCCCTGTCGACCGCATGCGCTTACGCTGCT 377
QY 180 GAAAGAAATCCCTTTAGACGTACCCAGCAGGTGTCATCAGCGCGCATTATAGCAATT 239
DB 378 CAAGAGAGAGCGCATCCCGCATCCCGACAGTCCGCCATGACAAAGGACAGCTCCAT 437
QY 240 GACTGTGACGCGCATCATCTATTTTCAGATACCGATCCCAATCGCTCATACGTTTC 299
DB 438 CCAGATCGACGCGCTCCCTACGTCAAGATTGTGATCCCTACCTTCTTCTATGTGT 497
QY 300 GAGCAATCAATTAATGCAATTAACCGCTTCCCAAGAGCGGTGCTCGTTATCGG 359
DB 498 GAGATTCATTAATTTTTCAGTCAATGAGCTTCCCAACATTAAGAGAGTGTGAG 557
QY 360 GCGTATGAGATTGACAAAGAGTTCGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 419
DB 558 AAGATTTACGTTAGCAAGAGATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 617
QY 420 CGCCCTCGATGAGAGCGCGCGGCTTGGGCTGTGAAAGTCTCCGTTACGAATCAAGAG 479
DB 618 GTCCATTATGAGAGCTGCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 677
QY 480 TTTGGTTCGCGCGAG 539
DB 678 TATATCTTCGCGAG 737
QY 540 AAAAGCGCGCGGTTATTCGAGATCCGAAAGCGCTTAAATCAAGAAATCACTTTCAG 599
DB 738 AAGAGTTCGCGAG 797
QY 600 TGTGACGCTGAG 659
DB 798 GGGTACGAGCTGAG 857
QY 660 GTCCATGCGAG 688
DB 858 CTGAGGCGCATGAG 886
RESULT 39
ADN97415 standard; DNA; 1071 BP.
XX
XX ADN97415;
XX
XX 29-JUL-2004 (first entry)
XX
XX Human SLP2 DNA for pain treatment.
XX
XX ds; gene; analgesic; gene therapy; neuronal mechano-transduction;
XX stomatin domain; current; voltage; plasma membrane; neuron; pain.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..1071
XX /*tag= a
XX
XX WO2004040299-A2.
XX
XX 13-MAY-2004.
XX

30-OCT-2003; 2003MO-BP012084.
 30-OCT-2002; 2002EP-00024474.
 30-OCT-2002; 2002US-0422098P.
 (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
 Lewin G, Heppenstall P, Eilers A;
 WPI; 2004-376269/35.
 P-PSDB; ADN97416.
 Identifying a compound capable of inhibiting the mechano-transduction of
 a neuron for treating pain by measuring the current or voltage at the
 plasma membrane of the cell contacted with the candidate compound.
 Disclosure; SEQ ID NO 13; 100pp; English.
 The invention relates to a method of identifying inhibitors of neuronal
 mechano-transduction by: (a) providing a cell over expressing a
 polypeptide comprising stomatin domain-containing proteins; (b)
 contacting the cell with a candidate compound; (c) measuring the current
 or voltage at the plasma membrane of the cell; and (d) identifying the
 candidate compound as an inhibitor of mechano-transduction if the current
 or voltage measured is altered in comparison to a control. The
 polynucleotide encoding the stomatin domain-containing protein, the
 polypeptide encoded by the polynucleotide, the cells over expressing the
 polypeptide comprising stomatin domain-containing proteins or the system
 is useful in identifying a compound capable of inhibiting the mechano-
 transduction of a neuron for preparing a composition for treating pain.
 This sequence corresponds to the human SLP2 DNA used in the invention.
 Sequence 1071 BP; 252 A; 293 C; 316 G; 210 T; 0 U; 0 Other;
 Query Match 16.4%; Score 155.6; DB 12; Length 1071;
 Beef Local Similarity 50.6%; Pred No. 3.3e-36;
 Matches 432; Conservative 0; Mismatches 389; Indels 33; Gaps 1;
 62 TCATCCCGGAGGAGGAGTCAAGTGTGAAAGGCTGGGGGTTTCATCGGCGCTGA 121
 119 TGTGCGCGAGGAGGAGGCTGGGTGTGAGGAATGGGCGGATTCACCGGATCTCG 178
 122 CGGCGGTTTGAATATTTTGAATCCCTTATGACCGCGCTGCTACCCGATCGCTGA 181
 179 AACCTGGTTTGAACATCTTCATCCCTGTGTAGACCGGATCCGATATGTGCGAGATCTGA 238
 182 AAGAAATCCCTTGAAGGATACCGAGGAGTGTGATCAAGCGGATTAATAGCAATGA 241
 239 AAGAAATTTTCATCAAGTGTGAGCAAGTGGCTGTGACTTCGCAATGTAATCTGCG 298
 242 CTGTTGACCGGATCATCTATTTTCAGATTAACCGATCCCAACTCGCTCATAGGTTGA 301
 299 AATATGATGAGATGCTTTCATCTGCGATATGAGACCTTAAAGGAGTACGATG 358
 302 GCAACTACATTAATGCAATTAACCGCTTCCCAAGAGCGCTGCTTCCGTTATGCGC 361
 359 AAGACCTGAGTATGCGTCAACCACTAGTCAAAACAATGAGATCAAGAGCTCGGCA 418
 362 GATATGAGTTGAGCAAAAGCTTGAAGACGCGAACAATCAACAATACCGTGTCTCG 421
 419 AACTCTCTTGAGCAAAAGTCTTCGGAACGGAAGTCCGTAATGCGAGATTTGAGATG 478
 422 CCTCGATGAAGCGCGCGGCTTGGGGTGTGAAAGTCTCCGTTAGCAATCAAGATTT 481
 479 CCAATCAACAAGTGTGATGCTGTGGGTATCGCTGCTCCGTTATGAGATCAAGATTA 538
 482 TGGTTCGCGCGCAAGAAATCTTGGCGCAATGAGGACCAATTAACCGCGCAAGGAAA 541
 539 TCCATATGCGCAACCCCGGCTGAAGAGATTAATGAGATGAGGAGGAGGAGCGCGGA 598
 542 AACGCGCGCGTATTTGGCGAATCGGAAGCGGCTAAATTCAGAAACAACCTTGCGAGTG 601
 599 AACGGGCGCAAGTTTGAAGTCTGA-----GG 625

602 GTACGCGTGAAGCCGAAATTCACATCGAAGGCGAGCTCAGGCTCGTCAATGCGT 661
 626 GAGCCGAGAGTGGCCATCAATGTGGCAGAAAGGAGAAACAGGCCCAAGATCTCGGCT 685
 662 CCAATGCGGAGAAATTCGCGCGATCAACCGCGCAAGCGGAGCGGAATTCCTGCGCC 721
 686 CGAAGGAGAAAGGCTGAACAGATTAATCAGGCGAGGAGAGAGCCAGTGCAATTCG 745
 722 TTGTTGCGGAAAGCCATGCGGAGGATCCGTTCAATTTGCGCGCCCTTCAAAACCAAG 781
 746 CGAAGCGGAGGCTTAAGCTGAAGCTATTCGAATCTGCTGCGAGCTTGACACAACATA 805
 782 GCGGGCGGAGTCCGTCATCTGAAGATTGGGGAACAATAGCTAGCGGCTTCAACAATC 841
 806 ATGAGATGACAGACCTTCACTGACTGTGGCGGACAGATATGTACGCGCTTCCCAAC 865
 842 TTGCAAGAAAGCAATAGCTGATTAATGCGCGCAATGTTGCGGACATCGGCGAGCTGA 901
 866 TGCCCAAGAGATCCCAACACTATCTACTGCTCCCAACCGTGGGAGATGACACAGATGG 925
 902 TTTCTGCGGCGATG 915
 926 TGGCTCAGGCGCATG 939
 RESULT 40
 AAH13961
 ID AAH13961 standard; cDNA; 1244 BP.
 AAH13961;
 26-JUN-2001 (first entry)
 Human cDNA sequence SEQ ID NO:11009.
 Human; primer: detection; diagnosis; antisense therapy; gene therapy; ss.
 Human; primer: detection; diagnosis; antisense therapy; gene therapy; ss.
 Homo sapiens.
 EP1074617-A2.
 07-FEB-2001.
 28-JUL-2000; 2000EP-00116126.
 29-JUL-1999; 99JP-00248036.
 27-AUG-1999; 99JP-00300253.
 11-JAN-2000; 2000JP-00118776.
 02-MAY-2000; 2000JP-00183767.
 09-JUN-2000; 2000JP-00241899.
 (HELI-) HELIX RES INST.
 Oca T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 WPI; 2001-318749/34.
 Primer sets for synthesizing polynucleotides, particularly the 5602 full-
 length cDNAs defined in the specification, and for the detection and/or
 diagnosis of the abnormality of the proteins encoded by the full-length
 cDNAs.
 Claim 8; SEQ ID NO 11009; 2537bp + Sequence Listing; English.
 The present invention describes primer sets for synthesizing 5602 full-
 length cDNAs defined in the specification. Where a primer set comprises:
 (a) an oligo-dT primer and an oligonucleotide complementary to the
 complementary strand of a polynucleotide which comprises one of the 5602
 CC nucleotide sequences defined in the specification, where the
 oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 of an oligonucleotide comprising a sequence complementary to the

complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH016 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention

Sequence 1244 BP; 284 A; 327 C; 368 G; 265 T; 0 U; 0 Other;

Query Match 16.4%; Score 155.6; DB 4; Length 1244;
Best Local Similarity 50.6%; Pred. No. 3.6e-36;
Matches 432; Conservative 0; Mismatches 389; Indels 33; Gaps 1;

62 TCATCCCGCAGGAGATCCAGCTGTGCAAAAGGCTCGGCGTTTCATCGCGCTGA 121
153 TCGTCCCGCAGGAGGCTGGGTGTGAGCGAATGGGCGAATCCACCGAATCCTG 212
122 CGGCGGTTGAATTTTGAATTCCTTATGACCGGGTGGCCTTACCGCATTCGCTGA 181
213 AGCTGGTTGAACTCCCTCATCTGTGTAGACCGGATCCGATATGTGCAAGTCTCA 272
182 AAGAAATCCCTTAAAGCTACCCAGCAGCTGTCATCAGCGCGATTAATAGCAATTGA 241
273 AGGAAATGTGATCAAGCTGCTGAGCAGTGGCTGTGACTCTGCAATGTAATCTGC 332
242 CTGTGACGGCATCATTAATTTCAAGTAACCGATCCAAACTGCTCATACGTTTGA 301
333 AAATGATGAGTCTTAACTGCGCATCATGAGACCTTACAAAGCAAGCTACGTTG 392
302 GCAATCATATATGCAATTCAGCTTGGCCAAAGCAGCGTGGCTCCGTTATCGGGC 361
393 AGGACCTGAGTATCCGCTCAACCTAGCTCAAAACAACATGAGATGAGAGCTGGCA 452
362 GTATGAGTTGAGCAAAAGCTTGAAGACGCGAAGCAATCAACAGTACCGTCTCCG 421
453 AACTCTCTGAGCAAAAGCTTCCGGGAACGGAGTCCCTGATGCCAGATTTGTGATG 512
422 CCTTCGATGAAGCCCGCGGCTTGGGGTGTGAAGTCTCTCGTTACGAATCAAGATT 481
513 CCATCAACCAAGCTGTGATGCTGGGTATCCGCTGCTCGTTATGAGATCAAGATTA 572
482 TGGTTCCGCGCAAGAAATCTTCGCGCATGCAAGCAAAATTACCGCGCAAGCGGAA 541
573 TCATGTGTCACCCCGGGTGAAGAGTCTATGCAATGAGTGAGGCAAGCGCGGA 632
542 AACCGCCGATATTCGCAATCCGAAGCCGTAATCAATCAACTTGGCACTG 601
633 AACGGGCAAGTCTTAAGTCTGA-----GG 659
602 GTCAAGCTGAAGCCGAAATCCAAATCCGAAGCGAGGCTCAGGCTGCAATGCGT 661
660 GGACCCGAGAGTGGGCAATGTCGCAAGAGGAAAGAAACAGGCCCAAGATCCCTGGCCT 719
662 CCAATGCGGAAATTCGCGCATCAACCGCGCAAGGCGAAGCGGAATCCCTGGCGC 721
720 CGAAGCAGAAAGGCTGAACAGATTAATCAAGGAGGAGGCGCAGTCAAGTTCTGG 779
722 TTGTTCCGAAGCCCAATGCGCAAGCCATCCGTCATATTCGCGCCCTTCAAAACCAAG 781
780 CGAAGGCAAGGCTTAAGCTGAGTATTCGATCTGCTGCACTGACACAGATTA 839
782 GCGGGGCGGATGCGGTCAATCTGAAGATTCGGAACAAATACGTAAGCGCGTTCAACAATC 841
840 ATGGAATGACAGCACTTCACTGACTGTGGCGAGCAAGTATGTCAAGCGGTTTCCAAAC 899

Qy 842 TTGCAAGAAAGCAATACGCTGATTAAGCCGCCAATGTTGCCGACATCGGACGCTGA 901
Db 900 TGGCCAAAGACTCCAAACATTAATCTTACTGCGCTCCAAACCTGGGAGATGTACACAGCATGG 959
Qy 902 TTCTGCGCGGATG 915
Db 960 TGGCTCAGGCGCATG 973

Search completed: August 13, 2005, 23:29:22
Job time : 624 secs

3

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 13, 2005, 22:22:31 ; Search time 207 Seconds

(without alignment)
7493.673 Million cell updates/sec

Title: US-10-018-470A-16

Perfect score: 948
Sequence: 1 atgaatttcattatctt.....gcagcaaacgcgaataa 948Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 81813359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCUTS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	172	18.1	1419	4	US-09-602-777A-139
2	155.2	16.4	1188	1	US-08-781-562-2
3	153.2	16.2	4403765	3	US-09-103-840A-2
4	153.2	16.2	4411529	3	US-09-103-840A-1
5	141.4	14.9	963	4	US-09-543-681A-2806
6	130.2	13.7	951	4	US-09-489-039A-6125
7	113	11.9	1107	4	US-09-902-540-4035
8	113	11.9	24986	4	US-09-902-540-1200
9	104.2	11.0	840	4	US-09-902-540-6837
10	104.2	11.0	4026	4	US-09-902-540-571
11	96	10.1	870	4	US-09-328-352-126
12	84.6	8.9	885	4	US-09-540-236-1751
13	84.6	8.9	100848	4	US-09-596-002-39
14	77	8.1	558	4	US-09-252-991A-5885
15	70.4	7.4	532	4	US-09-621-976-1043
16	64.8	6.8	840	4	US-09-248-796A-2756
17	59	6.2	546	4	US-09-252-991A-5903
18	58.8	6.2	1338	4	US-09-252-991A-5987
19	58.8	6.2	1338	4	US-09-270-767-13578
20	58	6.1	420	4	US-09-370-767-15253
21	53.8	5.7	301	3	US-09-222-575-26
22	53.8	5.7	301	4	US-09-389-681-26
23	53.8	5.7	301	4	US-09-620-405B-26
24	53.8	5.7	301	4	US-09-339-338-26
25	53.8	5.7	301	4	US-09-433-826B-26
26	53.8	5.7	301	4	US-09-604-287A-26
27	53.8	5.7	301	4	US-09-285-480-26

ALIGNMENTS

28	53.8	5.7	301	4	US-09-834-759-26	Sequence 26, Appl
C 29	53.8	5.7	301	4	US-09-590-751A-26	Sequence 26, Appl
C 30	53.8	5.7	301	4	US-09-551-621-26	Sequence 26, Appl
C 31	51	5.4	1664976	4	US-08-916-421B-1	Sequence 1, Appl
C 32	51	5.4	1664976	4	US-09-692-570-1	Sequence 180, Appl
33	49.2	5.2	905	4	US-09-663-600A-180	Sequence 154, Appl
34	49.2	5.2	982	4	US-09-663-600A-154	Sequence 9, Appl
35	49.2	5.2	982	4	US-09-621-976-9	Sequence 60, Appl
36	49.2	5.2	1022	4	US-09-663-600A-60	Sequence 6989, Ap
37	42.4	4.5	1602	4	US-09-252-991A-6989	Sequence 7042, Ap
38	42.4	4.5	2187	4	US-09-252-991A-7042	Sequence 544, App
39	41.2	4.3	503	3	US-09-221-017B-544	Sequence 106, App
40	41.2	4.3	1031	1	US-08-181-271A-106	Sequence 106, App
41	41	4.3	1031	1	US-08-449-315-106	Sequence 106, App
42	41	4.3	1031	1	US-08-444-803-106	Sequence 106, App
43	41	4.3	1031	1	US-08-449-043-106	Sequence 106, App
44	41	4.3	1031	1	US-08-456-265A-106	Sequence 106, App
45	41	4.3	1031	1	US-08-455-416-106	Sequence 106, App

RESULT 1
US-09-602-777A-139
Sequence 139, Application US/09602777A
Patent No. 6831165
GENERAL INFORMATION:
APPLICANT: Pompejus, Markus
APPLICANT: Krogger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Habernauer, Gregor
TITLE OF INVENTION: CORYNBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
FILE REFERENCE: BGI-128CP
CURRENT APPLICATION NUMBER: US/09/602,777A
CURRENT FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: DE 19931636.8
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19932125.6
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932126.4
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932127.2
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932128.0
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932129.9
PRIOR FILING DATE: 1999-07-19
PRIOR APPLICATION NUMBER: DE 19932226.0
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932920.6
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19932922.2
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19932924.9
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19932928.1
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19932930.3
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19932933.8
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19932935.4
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19932973.7
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19933002.6
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19933003.4

PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19933005.0
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19933006.9
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19941378.9
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19941379.7
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19941380.8
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19941391.6
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19942088.2
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 442
SEQ ID NO 139
LENGTH: 1419
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
FEATURE:
NAME/KEY: CDS
LOCATION: (101)..(1396)
OTHER INFORMATION: RXA00152
US-09-602-777A-139

Query Match 18.1%; Score 172; DB 4; Length 1419;
Best Local Similarity 51.7%; Pred. No. 2.2e-41;
Matches 391; Conservative 0; Mismatches 365; Indels 0; Gaps 0;

12 CATTATCTTGTGGGAGCGGCTTTCGCGCTTCAATCTTGTGTCATCCCA 71
121 CATAGTTTCTGTGCTTGTGCGGTGTGATCAAGTCATAGCCGATGCCCA 180
72 GCAGAGTCCACGTTGCGAAAGCTCGGCGTTTCATGCGCCCTGACGCGGTTT 131
181 GGGTGAAGCCCGCATTTGAACGCTTGTAAGTACACCGGACCGTTTCAAGGTGCGCT 240
132 GAATATTTTGTATCCCTTATGACCGGTGCGCCATTCGCTGGAAGAAATCCC 191
241 GACCTGCTGTGCTTATTCGAGTACCGGAGTACCGCAAGATCGACCCGTCGCGGT 300
192 TTTAGACGTACCGACGAGTCTGTCATCAGCGCGATTAATGCAATGACTGTTGACG 251
301 GGTCTCATTTCCACCGCAGGCTGTATTAACCAAGACACCTGACCGTCATGATAT 360
252 CATCATCTATTTCGAATCCGATCCAAATCTGCTCATACGCTTGAAGCACTACAT 311
361 CGTGTGACCTTCCAAATCAAGAACGAGCGCCCATCTTACGCGCTGGAACAATCAT 420
312 TATGCAATTAACCGCTTGGCCAAACGACGCTGCTTCCGTTATCGGCGGTGAGATT 371
421 CGTGTGTGAGACGATTTCTGAGCAACCTTGACAGCTGTGCGATGACCT 480
372 GAACAAAGCTTTGAAGACGACGAAATCAACAGTACCGTCTCTCGCCCTGATGA 431
481 GGAAGAAACCTCATCTTCACTGAGCTGATCAACCGCGCTCTCGTGGCAGCTGATGC 540
432 AGCCGCGGCGCTTGGGCTGTGAAGTCTTCCTGTTACGAATCAAGATTTGTTCCGCC 491
541 AGCAACCAACCAATGGGCTGTGCGCATGACGCTGTGAACTTAAAGGCAATTTGCCCC 600
492 GCAAGAAATCTTGGCGCAATGACGACCAATTAACCGCGCAACCGCAAAACCGCGCCG 551
601 ACCATTCATCCAGCAATGATGAGAAACAGATGAAGACAGACCTGTGAAGACCGGCAC 660
552 TATTGCGCAATCCGAGGCGCTTAAATGAAACCAATCAACCTTGCAGTGCAGCTGA 611
661 CATTTTGCAGGAGAGCTCAGCGGAGGACGACATCAAAACTGCGGAAGGTGAAGACA 720
612 AGCCGAAATTCGAACATCCGAGGAGGCTCAGGCTCGGTCAATGCGTCAATGCGGA 671
721 AGCAAGATCTCTCAAGCTGAGGAGTGAAGACGACATCATCTCTGAACGAGAGACAGA 780

672 GAAATGCCCCGATCAACGCGCCAAAGCGAAATCCTGCGCTTGTTCGCA 731
781 AGCGCAAGCATATCTCTGCGCGCCGGAAGTGAACGCGCAGTAACTCTCAAGGCGCA 840
732 AGCAATGCCAGACCATCTGTAATTTGCCGCCG 767
841 GGGTGAAGCCCGACCAATCCAAAGTCAACGACG 876

RESULT 2
US-08-781-562-2
Sequence 2, Application US/08781562
Patent No. 5763589
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goll, Surya K.
TITLE OF INVENTION: NOVEL HUMAN MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FaelsSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781.562
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0181 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1188 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMEDIATE SOURCE:
LIBRARY: Consensus
CLONE: Consensus
US-08-781-562-2

Query Match 16.4%; Score 155.2; DB 1; Length 1188;
Best Local Similarity 50.5%; Pred. No. 2.3e-36;
Matches 431; Conservative 0; Mismatches 390; Indels 33; Gaps 1;

62 TCATCCCCACAGAGATCAAGTTCGAAAGCTCGGAGCTTTCATCGCCCTGA 121
182 TCGTCCGACAGAGAGGCTGTGTGAGAGCAATGGCCGATTCCACCGATCTCG 241
122 CGGCGGTTTGAATATTGATTCCTTTATGACCGCGTGCCTACCGCATTCGCTGA 181
242 AGCTGGTTTGAATCTCTATCTCTGTGTTAAGCCGATCCGATATGTGAGAGTCA 301
182 AAGAAATCCTTTAGAGTACCAAGCAGGCTGTCATCAACCGGATTAATGCAATTGA 241
302 AGGAAATTTGATCAAGTGTGAGAGTGTGAGATCTGACATGATTAATCTTGC 361

Qy	24	CTGTGACGGCAATCATCTATTTTCGAAAGTAACGATCCCAAACTGSCCTCAACGTTGCA	3010
Db	362	AAATCGATGAGATCTTCTTACTCGCGATATGGAACCTTTACAAGCAAGCTACGGTGG	4221
Qy	302	GCAACTACATTAATGAGCAATTTACCCAGCTTGCCCAACAGACGTGCGTTCCGTTATCGAGC	3611
Db	422	AGGACCTGTAGTATGCGGTCAACCGACTAGCTCAAAACAACATGAGATCAAGGCTCGGCA	4811
Qy	362	GTAATGAGTTTGACAAAACGTTTGAAGAACGGACGAAATCAACGTAACGTCGCTCCG	4221
Db	482	AACCTCTCTMTGACAAGAAAGTCTTCGGGAAACGGGAAGTCCCTGATATCCGACATTTGTGATG	5411
Qy	422	CCCTCGATGAAAGCGCGCGGGGCTTGGGGGGTGAAGTAAGTCTCTCGATGCAAAATCAAGATT	4811
Db	542	CCATCAACCAAGCTGTGACTGCTGCGGGATCCGCTGCTTNCGTTATAGATCAAGATA	6011
Qy	482	TGATTCCGCGCGCAAGAAATCTTTCGCGCAATGACAGCAACAATTAACCGCGCAACGCGAA	5411
Db	602	TTCATGTGCCACCCCGGGTGAAGAAAGTATATGACAGTGAAGTGAAGCAGAGCGCGGA	6611
Qy	542	AAGCGCGCGGTATTGCCGAATCCGAAGCGCGTAAATGCAACAATCAACTTGCAGTG	6011
Db	662	AACGGGCAACAGTTCTTAGAGTCTGA-----GG	6881
Qy	602	GTCAGCGTGAAGCGGAAATCCACCAATCCGAAGCGAGCGGCTCAGGCTCGGTCATGCGT	6611
Db	689	GGACCCGAGGTGGCGCATTAATGTGGCAAGAAAGGAAGAAACGGCCCAAGATCTGGCT	7481
Qy	662	CCAATGCGGAAATATGCGCCGATCAACCGCGCCAAAGCGGAAACGGAAATCCCTGCGCC	7211
Db	749	CCGAAAGCAAAAAGCTCGAAGACATTAATACAGCAGCAGAGAGAGGCAAGTCAAGTTCTGG	8081
Qy	722	TTGTTGCGGAAGCCCAATGCCGAAGCCATCCGTCAATATGCGCGCCCTTCAAAACCAAG	7811
Db	809	CGAAGGCCAAGGCTAAAGCTGAAGCTATTGCAATCCTGGCTCAGACTCTGACACAACTA	8681
Qy	782	GCGGGGCGGATGCGGTCATATGTAABATTTGCGGAACAATACGTACCGCGGTTCAACATC	8411
Db	869	ATGGAAGATGACGAGCTTCACTGACTGTGCGGAGAGATATGTCAGCGCGTTCTCCAAAC	9221
Qy	842	TTGCGCAAGAAAGCAATAGCGCTATTATGCCCGCCCAATGTTGCGGACATTCGAGACCTGA	9011
Db	929	TGGCCAAAGACTCCACACATATCTTACTGCTCTCCAAACCTGGCGATGTCAACAGCATGG	9881
Qy	902	TTTCTGCCGCGCATG 915	
Db	989	TGGCTCAGGCGCATG 1002	
RESULT 3			
US-09-103-840A-2			
Sequence 2, Application US/09103840A			
Patent No. 6294328			
GENERAL INFORMATION:			
APPLICANT: FLEISCHMAN, Robert D.			
APPLICANT: WHITE, Owen R.			
APPLICANT: FRASER, Claire M.			
APPLICANT: VENTER, John C.			
TITLE OR INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM			
FILE REFERENCE: 24366-2007.00			
CURRENT APPLICATION NUMBER: US/09/103,840A			
CURRENT FILING DATE: 1998-06-24			
NUMBER OF SEQ ID NOS: 2			
SOFTWARE: PatentIn Ver. 2.1			
SEQ ID NO 2			
LENGTH: 4403765			
TYPE: DNA			
ORGANISM: Mycobacterium tuberculosis			
FEATURE:			
OTHER INFORMATION: CDC 1551			
OTHER INFORMATION: "n" bases at various positions throughout the sequence			
OTHER INFORMATION: represent a, t, c or g			

Query Match	16.2%	Score 153.2	DB 3	Length 4403765
Best Local Similarity	50.0%	Pred. No. 3.9e-14		
Matches 383	Conservative 0	Mismatches 383	Indels 0	Gaps 0
QY	2	TGGAATTTTTCATTATCTGTGTGGACGACCGCTGCGCTTTTCGAGCTTCAAACTCTTGTGCG	61	
DB	1677551	TGCGTGTTCGCGCGCTCTCTGTATTTTGGCCATCATCGTGTGTGGCCAACTCGGTGGCGC	1677610	
QY	62	TCATCTCCCGACGAGGAAGTCCACGTTGTCCAAAGGCTCGGGCGTTTCATCGCGCTTGA	121	
DB	1677611	TGATCCCGACGAGCGGAGCGCGCGGTGATCCAGCGCGCTGCTGTATGTCGTAAGCTCA	1677670	
QY	122	CGCGCGGTTTGAATATTTTATTTATCTCCCTTTATGACCGCGCTGACCGCATTCGCTGA	181	
DB	1677671	GTGGGACAGTTGACGCTGTGTGTGTGCTGTATTCACGCGCTCGGGCTCGGTGTGAAGCTGC	1677730	
QY	182	AAGAAATCCCTTTTGAAGTACCGACCGACCGGTCTGATCAACGCGGATATATACCAATTGA	241	
DB	1677731	GGAGCGGGGTGTGTGTCTTTCGCGCGGACACCGGTGATCAACGAGAACTTGAACGCTGA	1677790	
QY	242	CTGTTGACGCGATCATCTTATTTCCAGTAACCGATCCCAACTCGCTCATACGTTTCCA	301	
DB	1677791	ACATCGAACACCGTGTCTACTTCCAGGTGACCGTTCCGACAGCGGCGGTGTACAGATCA	1677850	
QY	302	GCAACTACATATATGGAATTAACCAAGTTGCGCCAAAGAGAGCGTCTGCTTACGTTATCGGGC	361	
DB	1677851	GCAATTCATCTGTGTGGGTGGAAGAGTCAACACACACCTCTGCGAAGTTGTGCGCG	1677910	
QY	362	GTATGAGATTGGAACAAACGTTTGAAGAAAGCGACGAAATCAACAGTACCGTCTCCG	421	
DB	1677911	GGATGACGCTGACACAGCTTTGACCTCTGCTGTACACAGATCAACGCCAGCTGCGCGCG	1677970	
QY	422	CCCTGATGAGACCGCGCGGGCTTGGGGTGTGAAGTCTCTCCGTTACGAATCAAGATT	481	
DB	1677971	TTCTGATGAGGCGACCGCGCGCTGTGGGGTCTGCGGGTGGCGGGGTGAGACTGCGCAGCA	1678030	
QY	482	TGTTTCGCGCGCAAGAAATCTTCCGCGCATGACGAGCACAATTAACCGCGGAACGCGAAA	541	
DB	1678031	TGATTCGCGCGCTCTGATTTCAAGCGTGTGATGAAAAAGCAGATGAAGCGACCGGAGAGA	1678090	
QY	542	AAGCGCGCGGATTTGCGGAATCCGAGAGCGGTAAATTCGAACAAATCAACTTGGCCAGTG	601	
DB	1678091	AGCAGCGATGATTTCTGACCGCGCGAAGGTACCCGGAGGCGCGATTAACACAGGCCAGG	1678150	
QY	602	GTCACGCTGGAAGCCGAATCCACATTCGGAAGCGAGGCTCAGGCTCGGTCAATGCGT	661	
DB	1678151	GGCAAAAGCAGGCGCGAGTCTGTGCGCGCGCGAGGCGCGCAAGCAGGCGCGCATCTTGGCTG	1678210	
QY	662	CCAAATCCGAGAAATGCGCGCGCATCAACGCGCGCAAGCGCAAGCGGAATCCTTGGCGCC	721	
DB	1678211	CTGAGAGCGGATCGGCACTGTGATGTGTGCGCGCTCAAGGTGAGCGCGCGCGCTTACC	1678270	
QY	722	TTGTTGCGGAAGCCAAATGCGGAGCCCATTCGATCAAAATTTGCGCGCGC	767	
DB	1678271	TGCAAGGCGCAAGGCGAGGCGCAAGGCGCATTCGAGAAAGAGCTTGC	1678316	
RESULT 4				
US-09-103-840A-1				
Sequence 1, Application US/09103840A				
Patent No. 6294328				
GENERAL INFORMATION:				
APPLICANT: FLEISCHMAN, Robert D.				
APPLICANT: WHITE, Owen R.				
APPLICANT: FRASER, Claire M.				
APPLICANT: VENTER, John C.				
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM				
FILE REFERENCE: 2436-2007.00				
CURRENT APPLICATION NUMBER: US/09/103.840A				
CURRENT FILING DATE: 1998-06-24				

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1  NUMBER OF SEQ ID NOS: 2
2  SOFTWARE: PatentIn Ver. 2.1
3  SEQ ID NO 1
4  LENGTH: 4411529
5  TYPE: DNA
6  ORGANISM: Mycobacterium tuberculosis
7  OTHER INFORMATION: H37Rv
8  US-09-103-840A-1

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Query Match	16.2%	Score 153.2;	DB 3;	Length 441129;
Best Local Similarity	50.0%;	Pred. No. 3.9e-34;		
Matches 383;	Conservative	0;	Mismatches 383;	Indels 0;
			Gaps	0;

OY	2	TGAAATTTTTCATTATCTTGTTGGCAGCCGCGCGCTTTCGAGCTTCGAAATCCTTTGCG	61
Db	1677417	TGAGTTTTCGCGCGCTCCTGGTGAATTTTCGCAATCATCTGTGTGGCCAAAGTCGGTGGCGC	1677416
OY	62	TCATCCCCCAGAGAAAGTCCAGCTGTTCGAAAGGCTTCGAGCGTTTCATTCGCGCCCTGA	121
Db	1677477	TGATTCGCGAGCGGAGAGCGCGCGGTGATTCGAGCGGCTGGGTCCTATATGTCGAGGTCA	1677536
OY	122	CGCGCGGTTTGAATATTTTGAATTTCCCTTTATTCGACCGGTCGCTTACCGCATTCGGTGA	181
Db	1677537	GTGGGCAAGTTGACCGCTGTGGTGGCGTTTCATTCGACCGGTCGCGGCTTCGGGTGACCTGC	1677596
OY	182	AAGAAATCCCTTTAGACGTCACCCAGCCAGGCTCTCATTCACGCGGATTAATACGAATTGA	241
Db	1677597	GCGAGCGGGTGTGTCTGTTTCCGCGCCAGCCGGTGATTCGGAAGACAACTTGACGCTGA	1677656
OY	242	CTGTTGACGGCATCATCTATTTCCAGATTAACGATCCCAAACTCGCTCATACGGTTTGA	301
Db	1677657	ACATTCGACACCGTGTCTACTTCCAGGTGACCGTTCCGACAGCGCGGTTGACGATCA	1677716
OY	302	GCAACTACATTATGSCAAATTACCAAGCTTGGCCCAAAGACGCTTGGCTTCCGTTATCGGGC	361
Db	1677717	GCAATTTCATGTGGGGTTCGAAAGCTCACAACACACACCTTCGCGAACGTTGTCGGCG	1677776
OY	362	GTAATGAGTTTGAACAAAAGTTTGAAGAGACGACGAAATCAAGTACCGTCTCCG	421
Db	1677777	GGATGACGCTGAGCAGAGCTTTGACCTCGCTGACACAGATTAAGCCCAAGTGGCGGGCG	1677836
OY	422	CCCTCGATGAAAGCGCGCGGGCTTGGGGTGTGAAGTCTTCCTTCGTAAGAAATCAAGATT	481
Db	1677837	TTCTCGATGAGGCGACCGGCGCGCTGGGGTCTGCGGGTGGCGCGGGTGAAGTCGCGACA	1677896
OY	482	TGTTTCGCGCGCAAGAAATCCTTCGCGCAATGCAAGGCACAAAATTACCGCGCAACGCGAAA	541
Db	1677897	TGCAATCCGCGCGCGCTCGATTCAGCGCTTCGATGAGAAAGCAGATGAAGCCCAACGGAGGA	1677956
OY	542	AACCGCGCCGTAATTCGCGAATCCGAAAGCGGTAAATTCGAACAATCAACTTGGCCAGTG	601
Db	1677957	AGCAGAGCATATTTCTGACCGCCGAAAGGTACCCGGAGGCGGCGATTAACAGGCGCAGG	1678016
OY	602	GTCAGCGTGAAGCGGAAATCCCAAGATTCGAAAGCGAGGCTCAGGCTCGGTCATGCGT	661
Db	1678017	GGCAAAACACAGCGCGAGATCTGTGGCGCGCGAGGGGCGCAACAGGCGCGCATTTGGGTG	1678076
OY	662	CCAATGCGGAGAAATCGCCCGCATCAACGCGCCAAAGCGGAACGGAAATCCTTCGGGCC	721
Db	1678077	CTGAGGCGCGATCGGCACTTCGGAATGTGCGCGCTCAAGGTTGAACGCGCGCGCTTACC	1678136
OY	722	TTGTTTCCGAAGCAATGCGAGCAATCGGTCAAATTTGCCGCGC	767
Db	1678137	TGCAGGCGCAAGGCGCAGGCGCAAGGCAATTCGAGAAAGCTTTGCCGC	1678192

RESULT 5
 US-09-543-681A-2806
 ; Sequence 2806, Application US/09543681A
 ; Patent No. 6605709
 ; GENERAL INFORMATION:
 ; APPLICANT: GARY BRETTON
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS

```

?
? TITLE OF INVENTION:  DIAGNOSTICS AND THERAPEUTICS
?
? FILE REFERENCE:  2709.1002-001
?
? CURRENT APPLICATION NUMBER:  US/09/543,681A
?
? CURRENT FILING DATE:  2000-04-05
?
? PRIOR APPLICATION NUMBER:  US 60/128,706
?
? PRIOR FILING DATE:  1999-04-09
?
? NUMBER OF SEQ ID NOS:  8344
?
? SEQ ID NO 2806
?
? LENGTH:  963
?
? TYPE:  DNA
?
? ORGANISM:  Proteus mirabilis
?
US-09-543-681A-2806

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Query Match	14.9%	Score 141.4;	DB 4;	Length 963;
Best Local Similarity	-52.7%;	Pred. No. 2.9e-32;		
Matches 307;	Conservative	0;	Mismatches 276;	Indels 0;
				Gaps 0;

OY	87	TGTGAAAGGCTCGGGCGCTTCCAAATCGGCGCCCTGACGGCCGGTTGAATATTTTGATTC	146
Db	129	TGTGAGGCTTTTGGACGTTATACACGTAACCCCTTGCTCCAGCCCTCAACCTCCTATTCC	188
OY	147	CTTATCGACCGCGTGGCTTACCGCCATTCGCTGAAAGAAATCCCTTTAGAGTACCGAG	206
Db	189	ATTATATTGACCGTATTTGGTGTGCTGATTAATATGATGGAAACAAGTATAGATATCCCTTC	248
OY	207	CCAGGTCTGCATCACGCGCGATTAATAGCAATTGACTGTGACGGCATCATCTATTTC	266
Db	249	TCAGAAAGTGAATTTCTCGTGAATATGCCAAATGTCAGTATTAATGCGGTCTGCTTATTCA	308
OY	267	AGTAACGATCCCAAACTCGCCTCATACGGTTGCGACACTACATTAATGACCAATACCCA	326
Db	309	AGTATATCATCTAGTAATAAGCTGCTTATAGAGTGAATAACTAGAGCTTGCATATATCA	368
OY	327	GCTTGCCCAAACGACGCTGCGTCCGTTATCGGCGGTATGAGATTGACAAACGTTTGA	386
Db	369	TCTAAAGCTAACCAATATCCGTACTGTGTATAGGCTCTATGGAACGTGATGAAATCTTTC	428
OY	387	AGAAACGACCAATCAACAGTACCGTGTCTCCGCGCTCGATGAAGCCGCGGGCTTG	446
Db	429	ACAACGTATCAGATCAATACCCGTTTATCTGATTTGTATGATGCACTMAACCCATG	488
OY	447	GGGATGAAATCCCTCGGTTACGAATCAAGATTTGGTCCGCGCAAGAAATCCTTCG	506
Db	489	GGGATTTAAATTAACCGTATTGAATTCGTGATGTGGCCCAACCAAGAGCTAATTTTC	548
OY	507	CGCATGCGAGCACAATTAACCGCGCGAACGCGAAMAAACGCGCCGCTATTGCGAAATCCGA	566
Db	549	TGCATGATATCGGACGATGAAGAGTGAGCGTAACTTAAGGTGTGATATTCTTAAGACAGA	608
OY	567	AGGCGGTAAATCGAACAAATCAACTTTGCCAGTGTGAGGCTGAAGCCGAAATCCACA	626
Db	609	AGGTATCCGTCAAGGCGCAATCTTAAAGCGAAGSTAAAMAAACAAGGGCAAAATCTTAA	668
OY	627	ATCGAAGGAGGCTCAGCGTGGGCGTCAATGCGTCAATGCG	669
Db	669	AGCAGAGGTAAAGTCAAGTCTGCTTTTTCACAGCCGAAGCC	711

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RESULT 6
US-09-489-039A-6125
; Sequence 6125, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489.039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 6125

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LENGTH: 951
TYPE: DNA
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-6125

Query Match 13.7% Score 130.2; DB 4; Length 951;
Best Local Similarity 51.1%; Pred. No. 6,8e-29;
Matches 294; Conservative 0; Mismatches 273; Indels 0; Gaps 0;

```
QY 88 GTGGAAGGCTTGGGCGTTTCCATCGCGCTGACGCGCGGTTGAATTTGATTC 147
DB 124 GTGGAAGGCTTGGGCGTTTCCATCGCGCTGACGCGCGGTTGAATTTGATTC 183
QY 148 TTTATGACCGCGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCGCTT 207
DB 184 TTTATGACCGCGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCGCTT 243
QY 208 CAGGCTGTGATCAGCGCGCTTACCGCTTACCGCTTACCGCTTACCGCTTAC 267
DB 244 CAGGAGGTTATCTCCCGGATTAACCGCTTACCGCTTACCGCTTACCGCTT 303
QY 268 GTTACCGATCCCAAACTCGCTTATACCGCTTACCGCTTACCGCTTACCGCT 327
DB 304 GTGATGACCGCGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCGCTT 363
QY 328 CTTCGCGCAAGCAGCGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCG 387
DB 364 CTGACGATGACCAACATCCGCTTACCGCTTACCGCTTACCGCTTACCGCTT 423
QY 388 GAAAGCGAAGCAATCAAGTACCGCTTACCGCTTACCGCTTACCGCTTACCG 447
DB 424 CAGCGGACGAGATTAACCGCTTACCGCTTACCGCTTACCGCTTACCGCTT 483
QY 448 GGTGTAAGTCTTCCGTTACCGCTTACCGCTTACCGCTTACCGCTTACCGCT 507
DB 484 GGGGTGAATTAACCGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCGCT 543
QY 508 GCAATGACGACCAATTAACCGCTTACCGCTTACCGCTTACCGCTTACCGCT 567
DB 544 TCGATGAAGCGCGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCGCT 603
QY 568 GCGCGTGAATTAACCGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCG 627
DB 604 GGGGTGCGACGCGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCGCT 663
QY 628 TCCGAAGCGGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCGCTTAC 654
DB 664 GCGGAGGCGGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCGCTTAC 690
```

RESULT 7
US-09-902-540-4035
Sequence 4035 Application US/0902540

Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 4035
LENGTH: 1107
TYPE: DNA
ORGANISM: Myxococcus xanthus
US-09-902-540-4035

Query Match 11.9%; Score 113; DB 4; Length 1107;

Best Local Similarity 51.1%; Pred. No. 1.1e-23;
Matches 266; Conservative 0; Mismatches 255; Indels 0; Gaps 0;

```
QY 216 CATCAGCGCGCTTATTAACGATTAACGATTAACGATTAACGATTAACGAT 275
DB 264 CATCAGCGCGCTTATTAACGATTAACGATTAACGATTAACGATTAACGAT 323
QY 276 TCCGAAGCGGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCGCTTAC 335
DB 324 GCGCGGAGGCGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCGCTTAC 383
QY 336 AACGAGCGGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCG 395
DB 384 GACGAGCGGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCG 443
QY 396 GCAATTAACGATTAACGATTAACGATTAACGATTAACGATTAACGATTAAC 455
DB 444 GACGCTCAACCAAGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCGCT 503
QY 456 AGTCTCGCTTACGAAATCAAGATTAACGATTAACGATTAACGATTAACGAT 515
DB 504 GGTGACGCGCTTACGATTAACGATTAACGATTAACGATTAACGATTAACGAT 563
QY 516 GGCACAAATTAACGCGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 575
DB 564 CAGCAGATTAACGCGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 623
QY 576 AATGCAACCAATTAACGCGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 635
DB 624 GCGCGCGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCGCT 683
QY 636 CAGGCTCAGGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCG 695
DB 684 CCAAGCGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 743
QY 696 CAAAGCGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 736
DB 744 GGAAGCGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 784
```

RESULT 8

US-09-902-540-1200
Sequence 1200 Application US/0902540

Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1200
LENGTH: 24986
TYPE: DNA
ORGANISM: Myxococcus xanthus
US-09-902-540-1200

Query Match 11.9%; Score 113; DB 4; Length 24986;
Best Local Similarity 51.1%; Pred. No. 4.5e-23;
Matches 266; Conservative 0; Mismatches 255; Indels 0; Gaps 0;

```
QY 216 CATCAGCGCGCTTATTAACGATTAACGATTAACGATTAACGATTAACGAT 275
DB 9409 CATCAGCGCGCTTATTAACGATTAACGATTAACGATTAACGATTAACGAT 9468
QY 276 TCCGAAGCGGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCGCTTAC 335
DB 9469 GCGCGGAGGCGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCGCTTAC 9528
```


APPLICANT: Paterson, Chandra
APPLICANT: Beig, Kim, L.
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
FILE REFERENCE: PM-0008-4 US
CURRENT APPLICATION NUMBER: US/09/596,002
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: 60/140,121
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PERL Program
SEQ ID NO 39
LENGTH: 100848
TYPE: DNA
ORGANISM: M. catarrhalis
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Inocyte template ID No. 6632636 39
PUBLICATION INFORMATION:
US-09-596-002-39

Query Match 8.9%; Score 84.6; DB 4; Length 100848;
Best Local Similarity 47.9%; Pred. No. 3e-14; Mismatches 264; Indels 0; Gaps 0;
Matches 243; Conservative 0;

QY 109 CATCGCGCCCTGACGCGGTTTGAATATTTGATTCCTTTATCGACCGCTCCCTAC 168
DB 15208 CACCAAACTTGAACCGGCTGAATTTTATTTCTTATGAGATGCTGCTAT 15267
QY 169 CGCCATGCTGGAAGAAATCCCTTTAGACGACCGAGGTCTGCATCAGCGCGAT 228
DB 15268 AAAGTACCAACCAAGACATCTTACTGATATCCCAAGCAAGAGTCAATACGGGTAT 15327
QY 229 AATACGCAATGACGTTGACGCGATCATCTATTTCCAAGTAAACCGATCCCACTCGC 288
DB 15328 AATGTCATATGATGCCAATCAGTGGCATATTAATTTGTCAGCTTGAGCATGA 15387
QY 289 TCATACGCTGACGACATCAATTATGCAATTAACCAAGCTTCCCAACGACGCTGCT 348
DB 15388 GTCATGCGATGGAATATTAACATGCGATTCGTAATTTGGTCAAAACATCCTTAAGC 15447
QY 349 TCCGTTATCGGCGGATGATGACAAACGTTTGAAGAACGCGAGCAATCAACGT 408
DB 15448 TCTATCATCGGAGATGATTTGATGCGGCTTATCCAGTCGACCAATTAACGA 15507
QY 409 ACCGTCGTCGCGCTCGATGAGCGCGCGGCGTGGGCGTGAAGATCTCCGTTAC 468
DB 15508 CAGCTAAAACGCGATCAGTATGATCATTTTGTGTTGGGAATTAACCTTAACCTGTG 15567
QY 469 GAATCAAGATTTGTTCCGCGCAAGAAATCTTCGCGCAATGCAAGCACAATTAAC 528
DB 15568 GAATCAAGATCAATCAAGCATCAGGACATGATTTGGATGAGAGCAAGCGGC 15627
QY 529 GCCGAACGCAAAACGCGCGCTTATTTGCCAATCCGAAGCGCGTAATCAACAATC 588
DB 15628 GCTGCGCTCAACGCGCTGCGCACCGCTCACCCGTCGATGTCAAACCAACCGCATC 15687
QY 589 AACCTGCGAGTGTGAGGTGAGGC 615
DB 15688 TTAGAAGCATGCGCGCTTAGAGGC 15714

RESULT 14
US-09-252-991A-5885
Sequence 5885, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 5885
LENGTH: 558
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5885

Query Match 8.1%; Score 77; DB 4; Length 558;
Best Local Similarity 49.7%; Pred. No. 5.3e-13; Mismatches 250; Indels 4; Gaps 2;
Matches 251; Conservative 0;

QY 9 TTTCATTTCTTTGTCAGCGCGTTCGCTTTGCGGCTTCAATCTTTGTGTCATCC 68
DB 30 TTGGCGATTTGCTGCTGTTCTTCGCGCTGCTGCTGTCAGCGCGCTGCGCATCTCCG 89
QY 69 CCAGAGAGAGTCCACGTTGCGAAGGCTCGGCGTTTCATGCGCGCTGACGCGCG 128
DB 90 CGAGTACGAGCGCGCGCTGCTGCTTCAGCTCGCGGCTTTCGAAGGTCAAGGCGCGG 149
QY 129 TTGAAATTTTGAATCCCTTTATCGACCGGCTGCGCTTACCGCATTCGTGAAGAAAT 188
DB 150 GCTGCTGCTGATTCGCGGATCCAGCATGCG--TGCGATCGACCTGCGCACCAT 206
QY 189 CCTTTAGACGTACCGACGAGTCTGCATCAGCGCGATTAATACGCAATTAAGTTGA 248
DB 207 GCTCTGACGCTGCGCGCGAGATGATTTCCCGCAACAGTTTCGTTGAAGTTCA 266
QY 249 CGGATCATTTATTTCCAGTACCGATCCCAACTCGCTCATTA--CGTTGAGCAACT 307
DB 267 CGCGGTGATGATTCGCGCTGCTGATCCGAGAAAGGCGATCATCAGGTGAGAACT 326
QY 308 ACATTATGCAATTAACCAAGTTCGCAAGAGAGCGTCCGTTATCGGGGATAG 367
DB 327 ACTGCGCGTCAACGACGATGTTGCGCGACACCTGCGCGGTGCTGCGCAAGC 386
QY 368 AGTTGACAAACGTTTGAAGAACGCGACGAATCAACAGTACGCTGCTCCGCTCG 427
DB 387 AGCTGACGAGATGCTGCGCGAGCGCGCGCTGACCTGAGATTCAGCAAGTCTCG 446
QY 428 ATGAAGCGCGCGGCTTGGGCTGTGAAGTCTCCGTTACGAATCAAGATTTGTTTC 487
DB 447 ATGCGACACGACGCGCTGCGGCGATCAAGGTGCGAATGTAAGATCAAGACGTCATC 506
QY 488 CGCGCAAGAAATCTTCGCGCAT 512
DB 507 TCAACGAATGATGTTGCGCAT 531

RESULT 15
US-09-621-976-1043
Sequence 1043, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 1043
LENGTH: 532
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 363..530
US-09-621-976-1043

Query Match 7.4%; Score 70.4; DB 4; Length 532;
Best Local Similarity 51.1%; Pred. No. 5e-11;
Matches 187; Conservative 1; Mismatches 177; Indels 1; Gaps 1;

QY 62 TCATCCCCAGAGAAAGTCAAGTTCGAAAGGCTGGGGGTTTCATCGGCGCTTA 121
DB 153 TGTGCGCGAGAGAGGCTGGGAGTGGAGCAATGGGCGGATTCACCGGATCTCG 212
QY 122 CGGCGGTTGAAATTTTGAATTCCTTTATCGACCGCGT-CGCCACCGCAATTCGCTG 180
DB 213 ACCCTGTTGAACATTCCTCATCCGTGTATASACCGGATCCGATATGAGAGTCTC 272
QY 181 AAGAATCCCTTGAAGCTTACGACCGGCTGCTGATCAAGCGGATTAATACCAATTG 240
DB 273 AAGAAATTTGATCAACCTGCTGAGCAGTGGCTGTGATCTTCACAAATTTACTCTG 332
QY 241 ACTGTTGAGGAGATCATATTTTCCAAAGTAACCGATCCAAACTGGCTCATACGGTTG 300
DB 333 CAATTCGATGAGTCTCTTACCTGCGCATATGAGACCTTTACAGGCAAGCTAGGTGTG 392
QY 301 AGCACTACATTTATGCAATTAACCCAGCTTGCCCAACGACGCTGCTTCCGTTATCGG 360
DB 393 GAGGACCCGAGATATCCCTGACCCGCTAGCTCAAAACATGATCAGAGCTCGG 452
QY 361 CGTATGAGTTGACAAACGTTTGAAGAACGCGACGAAATCAACATACCTGCTCTCC 420
DB 453 AAACCTCTCTGGAACAAAGCTTCCGGGGAACGAGTCCCTGAATCCAGCATTTGTGAT 512
QY 421 GGCCTC 426
DB 513 GCCATC 518

RESULT 16

US-09-248-796A-2756
; Sequence 2756, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248.796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074.725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096.409
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 2756
; LENGTH: 840
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-2756

Query Match 6.8%; Score 64.8; DB 4; Length 840;
Best Local Similarity 48.4%; Pred. No. 3e-09;
Matches 211; Conservative 0; Mismatches 222; Indels 3; Gaps 1;

QY 65 TCCCCAGAGAGATTCAGCTTGTGCAAAAGCTGGGCGTTTCATCGCGCCCTGACGG 124
DB 359 TACCAACAAGAGAGCTTGATAGTAAAGAAATGGGTAGTTCCATCGTATTTTGCTC 418
QY 125 CGGCTTGAATTTTGAATTCCTTTATCGACCGCGCTACCGCATTCGCTGAAAG 184
DB 419 CTGATTTAGCTATTTTGAATTCCTTTATTAATAACAGTTATGTTCAAAATTTAAAG 478
QY 185 AAATCCCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 244
DB 479 AAATGATTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 538
QY 245 TTGACGCGATCATCTATTTTCAAGTAAACGATCCCAAACTCGCTCATACGTTTCAAGCA 304

DB 539 TAAATGAATATATATATTAATAATCAATTCATATTAAGCAAGTATGAAATTGACG 598
QY 305 ACTACATTAATGCAATTAACCAAGCTTGCCCAAGACAGCGTGGTTCGTTATCGGCGCA 364
DB 599 ATTATTAATATTTCTATTAATAATTAATTAATTAATTAATTAATTAATTAATTAAT 658
QY 365 TCGAGTTGAGCAAAACGTTTGAAGACGCAAGAAATCAACAGTACCGTCTCGGCC 424
DB 659 TAGAATTAATCGAAATTTTGAAGAAATCGGAATTTTAATGATTAATTTGTTAAATTA 718
QY 425 TCGATGAAGCCCGCGGCG---CTTGAGGTGTGAAGTCCCTCGTTACGAATCAAGATT 481
DB 719 TTAATGAAGCAATGAGAAATTTGGGGATTGAATGATTAATTAATTAATTAAGATA 778
QY 482 TCGTCCCGCGCAAG 497
DB 779 TTATCCCAACACAAA 794

RESULT 17

US-09-252-991A-5903
; Sequence 5903, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074.788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094.190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5903
; LENGTH: 546
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5903

Query Match 6.2%; Score 59; DB 4; Length 546;
Best Local Similarity 51.3%; Pred. No. 1.4e-07;
Matches 137; Conservative 0; Mismatches 130; Indels 0; Gaps 0;

QY 304 AACTACATTAATGCAATTAACCAAGCTTGCCCAACGACGCTGCTTCCGTTATCGGCGCT 363
DB 64 AACTACCTGCGCGCCGACGACGAGTTGGCCGACCAACCTGCGCGGTGCTGGCAAG 123
QY 364 ATGAGTTGACAAACGTTTGAAGAACGCGACGAAATCAACATACCTGCTCTCGCC 423
DB 124 CACGAGCTGACGAGATGCTCGCCGAGCGCGCTCAACCTGATATTCAGCAAGTG 183
QY 424 CTGATGAAGCCCGCGGCTTGAGAGTGAAGTCTCGTTACGAATTAAGAAATTTG 483
DB 184 CTGATGCGCAGACGACCGCTGCGCATCAAGTGGCAATGTGAATTAACGACGCTC 243
QY 484 GTTCCGCGCAAGAAATCTTGGCGCAATGACGCAATTAATCCCGCAAGCGCAAAA 543
DB 244 GATCTCAAGATCAATGATGTTGCGGCATCGCCGCGCAGCGAGCGGAGGTGAGCGC 303
QY 544 CGGCGCGGATTTGCGCAATTCGAAGGC 570
DB 304 AGGCGCAAGTATCATCAGCCGAGGCG 330

RESULT 18

US-09-252-991A-5987/c
; Sequence 5987, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.

;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;; FILE REFERENCE: 107196.136
;; CURRENT APPLICATION NUMBER: US/09/252,991A
;; PRIOR FILING DATE: 1999-02-18
;; PRIOR APPLICATION NUMBER: US 60/074,788
;; PRIOR FILING DATE: 1998-02-18
;; PRIOR APPLICATION NUMBER: US 60/094,190
;; PRIOR FILING DATE: 1998-07-27
;; NUMBER OF SEQ ID NOS: 33142
;; SEQ ID NO 5987
;; LENGTH: 648
;; TYPE: DNA
;; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5987

Query Match 6.2%; Score 59; DB 4; Length 648;
Best Local Similarity 51.3%; Pred. No. 1.5e-07;
Matches 137; Conservative 0; Mismatches 130; Indels 0; Gaps 0;

QY 304 AACTACATTATGCGCAATTACCGAGCTTGCCCAACGACGCTGCGTTCCGTTATCGGGCGT 363
DB 588 AACTACCTGGCGCGCCAGCCAGATTGGCCACACACCTGCGCGCGCTGCTGGGCAAG 529
QY 364 ATGAGTTGACAAACGTTTGAAGACGCGACGAATCAACAGTACCGTCTCCGCC 423
DB 528 CACGAGCTGACAGAGATGCTGCGCGAGCGCGCTGAACCTGATATCCAGCAAGT 469
QY 424 CTCGATGAAGCCCGCGGGCTTGGGGTGTGAAGTCTCCGTTACGAATCAAGATTG 483
DB 468 CTCGATGGCGACGACCGCGCTGGGGCATCAAGGTGGCAATGTGAATCAAGCAGTC 409
QY 484 GTTCCGCGCAAGAAATCTTTCGCGCAATGACGAGCAAAATTAACGCCGAAACGCAAAA 543
DB 408 GATCTCAACGAATCATGATGTTGCGCCCATCGCCCGGACGCGGAGCGGAGCGTGAAGCC 349
QY 544 CGCGCCCGTATTCGGAATCCGAAGGC 570
DB 348 AGGCGCAAGTGATCATGCGGAGGC 322

RESULT 19
US-09-270-767-13578
; Sequence 13578, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13578
; LENGTH: 1338
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: n means any nucleotide
US-09-270-767-13578

Query Match 6.2%; Score 58.8; DB 4; Length 1338;
Best Local Similarity 47.0%; Pred. No. 2.4e-07;
Matches 180; Conservative 0; Mismatches 203; Indels 0; Gaps 0;

QY 188 TCCCTTAGAGTACCCAGCCAGTCTGCAATCAGCGCGATTAATACGAATTGACTGTG 247
DB 687 TCTCTTGAAGTGCGCGCGAGAGTGCTCTCAAGAACTCGGTACTGTGACGCTAG 746
QY 248 ACGGATATCTATTTCCAGTAACGATCCGAACCTGCGCTCATACGTTGACCACT 307
DB 747 ATGGGTTGCTACTACGCAATCAGCAATCCCTCAAGGCGGTATCAAGGTGTAACAAT 806

QY 308 ACATTATGCAATTACCAAGCTTGCCCAACGACGCTGCGTTTCGTTATCGGGGCTATG 367
DB 807 ACAGCAATTCAGCAAGTCTCTGCGGCGCACCACTGCGCAATGTGCTCGGCACAGAA 866
QY 368 AGTTGACAAACGTTTGAAGACGCAAGAAATCAACAGTACCGTGTCTCCGCCCTCG 427
DB 867 ATCTGTCCGACCTCTGACCCGAACGACCAATCTGCACACATGCAATGTCTCCG 926
QY 428 ATGAAGCCGCGGGGCTTGGGGTGTGAAGTCTCCGTTACGAATCAAGATTGTTTC 487
DB 927 ACNAGGCCACCGATTCCTCGGGGCGTTAAGTGAAGCCGTGGAATCAAGACGATTCCT 986
QY 488 CGCGCAAGAAATCTTTCGCAATGCAAGCACAAAATTAACCGCAACGCAAAAACGCG 547
DB 987 TGCCAATGCTCTCAGCGGGCGATGCGCGGAGCGAGGACGAGGAGCGCGCG 1046
QY 548 CCCGATTCGCAATCCGAAGGC 570
DB 1047 CCAAGTCAATTGCGCGAGGC 1069

RESULT 20
US-09-270-767-15253/C
; Sequence 15253, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15253
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-15253

Query Match 6.1%; Score 58; DB 4; Length 420;
Best Local Similarity 52.5%; Pred. No. 2.4e-07;
Matches 127; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 328 CTTCGCCCAACGACGCTGCGTTATCGGGGTAATGAAGTGAACAAACGTTTGA 387
DB 374 CTGGCAACGATATCTTACGAGGCAATGGAACTGGGATTTGATGAATCTAGC 315
QY 388 GAAGCGACGAATCAACAGTACCGTGTCTCCGCCCTCGATGAAGCCCGGGGCTTGG 447
DB 314 GAGGTATGACGATTTCCGCAATGCAAGTTCACTGACGAAGCCACCGATGCCCTGG 255
QY 448 GGTGGAAGTCTCCGTTACGAATCAAGATTGTTCCGCGCAAGAAATCTTTCG 507
DB 254 GGCATCAAGTTGAAGTGTGGAATCAAGGTCTGCTGCTGCGCGGCACTCAAGCT 195
QY 508 GCAATGACGACAAATTAACCGCGAAGCGCAAAAACGCGCCGATATTCGAATCCGA 567
DB 194 GCAATGCGCGGAGGAGCAAGACCGCGGAAACCGCGCAAGTCAATGCGCGGAA 135
QY 568 CG 569
DB 134 GG 133

RESULT 21
US-09-222-575-26/C
; Sequence 26, Application US/09222575
; Patent No. 6387697
; GENERAL INFORMATION:
; APPLICANT: Yudiu, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun

;; TITLE OF INVENTION: Compositions for the Treatment and Diagnosis of Breast Cancer
;; FILE REFERENCE: 210121.470
;; CURRENT APPLICATION NUMBER: US/09/222,575
;; CURRENT FILING DATE: 1998-12-28
;; NUMBER OF SEQ ID NOS: 174
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 26
;; LENGTH: 301
;; TYPE: DNA
;; ORGANISM: Human
US-09-222-575-26

Query Match 5.7%; Score 53.8; DB 3; Length 301;
Best Local Similarity 51.9%; Pred. No. 3.8e-06;
Matches 121; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 607 CGTGAAGCCGAATCCACATCCGAAGCGGCTCAGGCTCGGTCAATGCGTCCAT 666
DB 233 CGAGAGTGGCCATCATGTGGCAGAGGAGAAACAGGCCAGATCTGCTCCGAA 174
QY 667 GCCGAAATGCGCGCATCAACCGCCCAAGGCGAAATCCCTGCGCTTGT 726
DB 173 GCAGAAAGGCTGCACATTAATAGGACAGAGAGGCCAGTCCAGTTCTGGCGAAG 114
QY 727 GCCGAAGCCAAATGCCAAGCCATCCGTCAATTCGCCGCCCTTCAACCCAGGCGG 786
DB 113 GCCAAGGCTAAAGCTGAAGCTATTGCAATCTGGCTGAGCTCTGACACACATATATGA 54
QY 787 GCGGATGCGGTCAATCTGAAGTTGGGAAACAATAGTACGCGCTTCAACA 839
DB 53 GATGAGCAGCTTCACTGACTGTGGCCGAGCAGTATGAGGCGCTTCCAA 1

RESULT 22
US-09-389-681-26/c
; Sequence 26, Application US/09389681A
; Patent No. 6518237
; GENERAL INFORMATION:
; APPLICANT: Yugui, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C3
; CURRENT APPLICATION NUMBER: US/09/389,681A
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-389-681-26

Query Match 5.7%; Score 53.8; DB 4; Length 301;
Best Local Similarity 51.9%; Pred. No. 3.8e-06;
Matches 111; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 607 CGTGAAGCCGAATCCACATCCGAAGCGGCTCAGGCTCGGTCAATGCGTCCAT 666
DB 233 CGAGAGTGGCCATCATGTGGCAGAGGAGAAACAGGCCAGATCTGCTCCGAA 174
QY 667 GCCGAAATGCGCGCATCAACCGCCCAAGGCGAAATCCCTGCGCTTGT 726
DB 173 GCAGAAAGGCTGCACATTAATAGGACAGAGAGGCCAGTGAAGTTCTGGCGAAG 114
QY 727 GCCGAAGCCAAATGCCAAGCCATCCGTCAATTCGCCGCCCTTCAACCCAGGCGG 786
DB 113 GCCAAGGCTAAAGCTGAAGCTATTGCAATCTGGCTGAGCTCTGACACACATATATGA 54
QY 787 GCGGATGCGGTCAATCTGAAGTTGGGAAACAATAGTACGCGCTTCAACA 839

DB 53 GATGAGCAGCTTCACTGACTGTGGCCGAGCAGTATGTCAGGCGCTTCCAA 1

RESULT 23
US-09-620-405B-26/c
; Sequence 26, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-620-405B-26

Query Match 5.7%; Score 53.8; DB 4; Length 301;
Best Local Similarity 51.9%; Pred. No. 3.8e-06;
Matches 121; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 607 CGTGAAGCCGAATCCACATCCGAAGCGGCTCAGGCTCGGTCAATGCGTCCAT 666
DB 233 CGAGAGTGGCCATCATGTGGCAGAGGAGAAACAGGCCAGATCTGCTCCGAA 174
QY 667 GCCGAAATGCGCGCATCAACCGCCCAAGGCGAAATCCCTGCGCTTGT 726
DB 173 GCAGAAAGGCTGCACATTAATAGGACAGAGAGGCCAGTCCAGTTCTGGCGAAG 114
QY 727 GCCGAAGCCAAATGCCAAGCCATCCGTCAATTCGCCGCCCTTCAACCCAGGCGG 786
DB 113 GCCAAGGCTAAAGCTGAAGCTATTGCAATCTGGCTGAGCTCTGACACACATATATGA 54
QY 787 GCGGATGCGGTCAATCTGAAGTTGGGAAACAATAGTACGCGCTTCAACA 839
DB 53 GATGAGCAGCTTCACTGACTGTGGCCGAGCAGTATGTCAGGCGCTTCCAA 1

RESULT 24
US-09-339-338-26/c
; Sequence 26, Application US/09339338A
; Patent No. 6573368
; GENERAL INFORMATION:
; APPLICANT: Yugui, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C2
; CURRENT APPLICATION NUMBER: US/09/339,338A
; CURRENT FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-339-338-26

Query Match 5.7%; Score 53.8; DB 4; Length 301;
Best Local Similarity 51.9%; Pred. No. 3.8e-06;

Matches 121; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

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Oy 607 CGTGAAGCCGAATCCAAATCCGAGGCGGCTCAGGCTGCGTCAATGCGTCCAT 666
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 233 CGAGAGTGGCCATCAATGTGGCAGAGGAGAAAGAGCCAGATCTGGCTCCGAA 174
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 667 GCCGAGAAATCGCCCGCATCAACCGCCGAAAGCGGAGGGAATCCCTGGCCTTGT 726
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 173 GCAGAAAAGGCTGCACAGATTAATCAGGACAGAGAGGCCAGTGTGAGTTCGCGAAG 114
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 727 GCCGAGCAATGCCGAGCCATCCGTCAATTCGCCGCCCTTCAAAACCCAGGCGGG 786
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 113 GCCAAGGCTAAAGCTGAAGCTATTGCAATCTGGCTGACGCTTACCAACATTAATGA 54
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 787 GCGGATGCGTCAATCTGAAGATTGCGGAAACATATCGTAGCGGCTTCAACAA 839
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 53 GATGACAGAGCTTCACTGACTGTGGCCGAGCAGTATGTCAAGCGCTTCTCCAA 1
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 25

US-09-433-826B-26/c
; Sequence 26, Application US/09433826B
; Patent No. 6579973

; GENERAL INFORMATION:

; APPLICANT: Jiang, Yuqi

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Xu, Jianshun

; APPLICANT: Harlocker, Susan L.

; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND

; FILE REFERENCE: 210121.470C4

; CURRENT APPLICATION NUMBER: US/09/433,826B

; CURRENT FILING DATE: 1999-11-03

; NUMBER OF SEQ ID NOS: 474

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 26

; LENGTH: 301

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-433-826B-26

Query Match 5.7%; Score 53.8; DB 4; Length 301;
Best Local Similarity 51.9%; Pred. No. 3.8e-06;
Matches 121; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

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Oy 607 CGTGAAGCCGAATCCAAATCCGAGGCGGCTCAGGCTGCGTCAATGCGTCCAT 666
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 233 CGAGAGTGGCCATCAATGTGGCAGAGGAGAAAGAGCCAGATCTGGCTCCGAA 174
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 667 GCCGAGAAATCGCCCGCATCAACCGCCGAAAGCGGAGGGAATCCCTGGCCTTGT 726
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 173 GCAGAAAAGGCTGCACAGATTAATCAGGACAGAGAGGCCAGTGTGAGTTCGCGAAG 114
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 727 GCCGAGCAATGCCGAGCCATCCGTCAATTCGCCGCCCTTCAAAACCCAGGCGGG 786
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 113 GCCAAGGCTAAAGCTGAAGCTATTGCAATCTGGCTGACGCTTACCAACATTAATGA 54
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 787 GCGGATGCGTCAATCTGAAGATTGCGGAAACATATCGTAGCGGCTTCAACAA 839
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 53 GATGACAGAGCTTCACTGACTGTGGCCGAGCAGTATGTCAAGCGCTTCTCCAA 1
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 26

US-09-604-287A-26/c
; Sequence 26, Application US/09604287A
; Patent No. 6586572

; GENERAL INFORMATION:

; APPLICANT: Jiang, Yuqi

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Xu, Jianshun

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS OF BREAST CANCER
; FILE REFERENCE: 210121.470C7

; CURRENT APPLICATION NUMBER: US/09/604,287A

; CURRENT FILING DATE: 2000-06-22

; NUMBER OF SEQ ID NOS: 489

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 26

; LENGTH: 301

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-604-287A-26

Query Match 5.7%; Score 53.8; DB 4; Length 301;
Best Local Similarity 51.9%; Pred. No. 3.8e-06;
Matches 121; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

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Oy 607 CGTGAAGCCGAATCCAAATCCGAGGCGGCTCAGGCTGCGTCAATGCGTCCAT 666
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 233 CGAGAGTGGCCATCAATGTGGCAGAGGAGAAAGAGCCAGATCTGGCTCCGAA 174
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 667 GCCGAGAAATCGCCCGCATCAACCGCCGAAAGCGGAGGGAATCCCTGGCCTTGT 726
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 173 GCAGAAAAGGCTGCACAGATTAATCAGGACAGAGAGGCCAGTGTGAGTTCGCGAAG 114
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 727 GCCGAGCAATGCCGAGCCATCCGTCAATTCGCCGCCCTTCAAAACCCAGGCGGG 786
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 113 GCCAAGGCTAAAGCTGAAGCTATTGCAATCTGGCTGACGCTTACCAACATTAATGA 54
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 787 GCGGATGCGTCAATCTGAAGATTGCGGAAACATATCGTAGCGGCTTCAACAA 839
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 53 GATGACAGAGCTTCACTGACTGTGGCCGAGCAGTATGTCAAGCGCTTCTCCAA 1
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 27

US-09-285-480-26/c
; Sequence 26, Application US/09285480
; Patent No. 6590076

; GENERAL INFORMATION:

; APPLICANT: Yuqi, Jiang

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; TITLE OF INVENTION: COMPOSITIONS OF BREAST CANCER AND METHODS FOR THEIR USE

; FILE REFERENCE: 210121.470C1

; CURRENT APPLICATION NUMBER: US/09/285,480

; CURRENT FILING DATE: 1999-04-02

; NUMBER OF SEQ ID NOS: 181

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 26

; LENGTH: 301

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-285-480-26

Query Match 5.7%; Score 53.8; DB 4; Length 301;
Best Local Similarity 51.9%; Pred. No. 3.8e-06;
Matches 121; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

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Oy 607 CGTGAAGCCGAATCCAAATCCGAGGCGGCTCAGGCTGCGTCAATGCGTCCAT 666
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 233 CGAGAGTGGCCATCAATGTGGCAGAGGAGAAAGAGCCAGATCTGGCTCCGAA 174
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 667 GCCGAGAAATCGCCCGCATCAACCGCCGAAAGCGGAGGGAATCCCTGGCCTTGT 726
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 173 GCAGAAAAGGCTGCACAGATTAATCAGGACAGAGAGGCCAGTGTGAGTTCGCGAAG 114
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 727 GCCGAGCAATGCCGAGCCATCCGTCAATTCGCCGCCCTTCAAAACCCAGGCGGG 786
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 113 GCCAAGGCTAAAGCTGAAGCTATTGCAATCTGGCTGACGCTTACCAACATTAATGA 54
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```

OY 787 GCGATGGCGCAATCTGAAGATTGCGGAAACAATACGAGCCGGCTTCAACA 839
Db 53 GATGACGAGCTTCACTGACTGTGGCCGAGCAGTATGTCAGCGGCTTCCAA 1

RESULT 28
US-09-834-759-26/c
; Sequence 26, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-834-759-26

Query Match 5.7%; Score 53.8; DB 4; Length 301;
Best Local Similarity 51.9%; Pred. No. 3.8e-06;
Matches 121; Conservative 0; Mismatches 112; Indels 0; Gaps 0

OY 607 CGTGAAGCGGAATCAATCCGAATCCGAGCGCTGCGGTGATCGTTCAT 666
Db 233 CGAGGTGCGCATCATATGTGGCAGAGGAAAGAAACAGGCCCATCTGTGGCTCCGAA 174
OY 667 GCGGAGAAATGCGCCCGCATCAACCGCGCCAAAGCGGAATCCCTGCGCTTTGT 726
Db 173 GCAGAAAGGCTGCGACAGATAATCAGCAGCAGGAGAGGACCATGCTTGGCGAAG 114
OY 727 GCGGAGCCATATGCGGAGCCATCCGTCAATTGCGCGCCCTTCAAAACCGAAGCGGG 786
Db 113 GCCAAGGCTAAAGCTGAAGCTATTCGAATCTGCGCTGCGAGCTCTGCACACACATATGGA 54
OY 787 GCGGATGCGCTCAATCTGAAAGTTGGGGAACAATNGTAGCCGCGCTTCAACA 839
Db 53 GATGACGAGCTTCACTGACTGTGGCCGAGCAGTATGTCAGCGGCTTCCAA 1

RESULT 29
US-09-590-751A-26/c
; Sequence 26, Application US/09590751A
; Patent No. 6756477
; GENERAL INFORMATION:
; APPLICANT: Yugu, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C6
; CURRENT APPLICATION NUMBER: US/09/590,751A
; CURRENT FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 479
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-590-751A-26

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[illegible]

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Patent No. 6503729
TITLE OF INVENTION: jannaschi
FILE REFERENCE: pb275
CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1664976
TYPE: DNA
ORGANISM: Methanococcus jannaschi
FEATURES:
NAME/KEY: misc feature
LOCATION: (28222)..(28222)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (98120)..(98120)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (98159)..(98159)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (98239)..(98239)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (98266)..(98266)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (98343)..(98343)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (148948)..(148948)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (163385)..(163385)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (191989)..(191989)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (191995)..(191995)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (231980)..(231980)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (234187)..(234187)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (234220)..(234220)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (234814)..(234814)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (309398)..(309398)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (309418)..(309418)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (312837)..(312837)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (312993)..(312993)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (319226)..(319226)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (559167)..(559167)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (559241)..(559241)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (600992)..(600992)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (622708)..(622708)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (657081)..(657081)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (657203)..(657203)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (674435)..(674435)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (682442)..(682442)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (713652)..(713652)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (779676)..(779676)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (871619)..(871619)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1084830)..(1084830)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1096846)..(1096846)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1119881)..(1119881)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1130881)..(1130881)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1313224)..(1313224)
OTHER INFORMATION: n equals a, t, c, or g
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/ NAME/KEY: misc.feature
/ LOCATION: (1349473)..(1349473)
/ OTHER INFORMATION: n equals a, t, c, or g
/ NAME/KEY: misc.feature
/ LOCATION: (1349491)..(1349491)
/ OTHER INFORMATION: n equals a, t, c, or g
/ NAME/KEY: misc.feature
/ LOCATION: (1470091)..(1470091)
/ OTHER INFORMATION: n equals a, t, c, or g
/ NAME/KEY: misc.feature
/ LOCATION: (1569020)..(1569020)
/ OTHER INFORMATION: n equals a, t, c, or g
/ NAME/KEY: misc.feature
/ LOCATION: (1602912)..(1602912)
/ OTHER INFORMATION: n equals a, t, c, or g
/ NAME/KEY: misc.feature
/ LOCATION: (1603734)..(1603734)
/ OTHER INFORMATION: n equals a, t, c, or g
/ NAME/KEY: misc.feature
/ LOCATION: (1637998)..(1637998)
/ OTHER INFORMATION: n equals a, t, c, or g
/ NAME/KEY: misc.feature
/ LOCATION: (1664854)..(1664855)
/ OTHER INFORMATION: n equals a, t, c, or g
US-08-916-4218-1
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Query Match 5.4%; Score 51; DB 4; Length 1664976;
Best Local Similarity 46.0%; Pred. No. 0.0014;
Matches 172; Conservative 0; Mismatches 202; Indels 0; Gaps 0;
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QY 196 GACGTACCCAGCCAGGCTGTCATCAGCGCGGATATACCGCAATTGACTGTTACGGCANTC 255
DB 724286 GATATCCCTCCCTCAAGAGATGATTACAAAGATAATGCAATTGTAAGGATGCGGAT 724227
QY 256 ATCTATTTCCAAAGTACCGATCCCAATCCCTCATAGCGTTGCGCACTACATTATG 315
DB 724226 GTTATATATAGGGTTATAGATGTTGAAAAGCAATTTAGAAATTGAGATTACGATAT 724167
QY 316 GCATTTACCCAGCTTCCCAACGACGCTGCTCCGTTACGGCGATGAGATTGAC 375
DB 724166 GCTATATATTAATCTAGCTCAACCACTAGGCGCAATATGTAATGATGATAGAT 724107
QY 376 AAAACGTTTGAAGACGCGAGCAATCAACAGTACCGCTCTCCGCCCTCGATGAACC 435
DB 724106 GAGGTTTAAATTAAGGAGATATATACTCAAGTTATGAAATTTTGGATAGAG 724047
QY 436 GCCGGGGCTTGGGGGTGAAAGTCCCTCCTTAGAAATCAAGATTGTTCCGGCGCA 495
DB 724046 ACGATGCAATGGGAGATTGAAAGGTTGAAAGTTAAAGAAATAGACCAACAG 723987
QY 496 GAAATCCTTCGCGCAATGACGACAAATTAACCGCGAAGCGGCGCGGAT 555
DB 723986 GACATTAATAATCCATGCTCAACAATAGAGGAGAGAGATTGAAAGAGAGCAAT 723927
QY 556 GCCGAATCCGAGG 569
DB 723926 TTAGAGGACAGAGG 723913
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RESULT 32
US-09-692-570-1/c
Sequence 1, Application US/09692570
Patent No. 6797466
GENERAL INFORMATION:
APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ
Patent No. 6797466
TITLE OF INVENTION: jamaeschi
FILE REFERENCE: PB275C1
CURRENT FILING DATE: 2003-01-14
CURRENT APPLICATION NUMBER: US/09/692,570
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
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PRIOR APPLICATION NUMBER: US 08/916,421
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1664976
TYPE: DNA
ORGANISM: Methanococcus jamaeschi
FEATURE:
NAME/KEY: misc.feature
LOCATION: (28222)..(28222)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc.feature
LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc.feature
LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc.feature
LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc.feature
LOCATION: (98120)..(98120)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc.feature
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LOCATION: (231980)..(231980)
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LOCATION: (657203)..(657203)
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LOCATION: (713652)..(713652)
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LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
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LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals a, t, c, or g
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NAME/KEY: misc feature
LOCATION: (779676)..(779676)
OTHER INFORMATION: n equals a, t, c, or g
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NAME/KEY: misc feature
LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a, t, c, or g
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OTHER INFORMATION: n equals a, t, c, or g
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NAME/KEY: misc feature
LOCATION: (1084830)..(1084830)
OTHER INFORMATION: n equals a, t, c, or g
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LOCATION: (1096846)..(1096846)
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NAME/KEY: misc feature
LOCATION: (1119881)..(1119881)
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LOCATION: (1130881)..(1130881)
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NAME/KEY: misc feature
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OTHER INFORMATION: n equals a, t, c, or g
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Query Match 5.4%; Score 51; DB 4; Length 1664976;
Best Local Similarity 46.0%; Pred. No. 0.0014;
Matches 172; Conservative 0; Mismatches 202; Indels 0; Gaps 0;

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QY 196 GACGTACCCAGCCAGCTGTCATCAACGGCGCATATACGAATTGACTTTGACGGCATC 255
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 724286 GATATCCCTCCTCAAGAGATGATTACAAAGGATATGCACTTGMAAGTGATGCGGTT 724227

QY 256 ATCTATTTCGAAGCAACGATCCCAACCTGCTCATACGGTTGAGCAATCATATG 315
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 724226 GTTATTATAGGGTTATATAGATTGMAAAGCAATTTTGAAGTTGAGATTACGAATAT 724167

QY 316 GCAATTACCCAGCTTGGCCCAACGACGCTGCTCCGTTATCGGCGATGAGTTGAC 375
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 724166 GCTATATATTAAGTTAGTCAACCAACCACTGAGGCAATTAATGTTAGTGAATGAT 724107

QY 376 AAAACGTTGAAGAACCGGACGAATCAACATGACCGTCTCCGCCCTCGATGAAGCC 435
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 724106 GAGCTTTTAATTAAGGAGGATATTAACCAAGTTATGMAATTTTGATGATGAGAG 724047

QY 436 GCCGGCGCTGGGGTGGAAGTCCTCCGTTAAGAAATCAAGATTTGGTTCCGCCGCA 495
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 724046 ACAGATGATGGGAGTTAGGATGAAAAGTTGAAGTAAATGACCCACAGAG 723987

QY 496 GAAATCCTTGCAGATGACGACGCAAAATTACCGCGAACGCAAAAACGCCCGCTGATT 555
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 723986 GACATTAATAATGCAATGCTCAACCAATGAGGACAGATGGAAGAGGACGACATA 723927

QY 556 GCCGATTCGAAGG 569
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 9
LENGTH: 982
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 72..944
NAME/KEY: sig_peptide
LOCATION: 72..197
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 7.1999980926514
OTHER INFORMATION: seq ILFSLFLVIT/FP
US-09-621-976-9

Query Match 5.2%; Score 49.2; DB 4; Length 982;
Best Local Similarity 49.6%; Pred. No. 0.00016;
Matches 126; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

QY 316 GCAATTACCCAGCTTGCCCAACGACGCTGCTTCCGTTATCGGGCGTATGAGTTGAC 375
DB 486 GCAACATTCTGCTGGCTCAACCACTCTGAGAAATGCTTAGGGACACAGACCTTGTC 545
QY 376 AAAAGCTTGAAGAACGCGACGAATCAACGTAACCGTCTCCGCCCTCGATGAAGCC 435
DB 546 CAGATCTTAGCTGACGAGAAAGATCGCCATCACTCCAGACTTTACTTGATATATCC 605
QY 436 GCCGGGCTTGGGGTGTGAAAGTCTCCTCGTTACGAATCAAGATTTGGTCCGCGAA 495
DB 606 ACCGACCTGTGGGGATCCGGTGGCCCGAGTGAATCAAGATTCGATTCGGTG 665
QY 496 GAAATCTTCCGCGAATGACGACAAATTACCGCGAAACGCGCCCGTATT 555
DB 666 CAGTTGACAGATCCATGCGACCGAGGCTGAGGCCACCCGGGAGCGAGCCAAAGTTC 725
QY 556 GCCGAATCCGAAG 569
DB 726 CTGCGAGCTGAAG 739

RESULT 36

US-09-663-600A-60
Sequence 60, Application US/09663600A
Patent No. 6573068
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duciart, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
FILE REFERENCE: 31.US3.CIP
CURRENT APPLICATION NUMBER: US/09/663,600A
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/191,997
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/081,563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/096,116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/099,273
PRIOR FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 229
SOFTWARE: Patent.pm
SEQ ID NO 60

LENGTH: 1022
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 112..237
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 7.1999980926514
OTHER INFORMATION: seq ILFSLFLVIT/FP
NAME/KEY: polyA_signal
LOCATION: 976..981
NAME/KEY: polyA_site
LOCATION: 1010..1022
US-09-663-600A-60

Query Match 5.2%; Score 49.2; DB 4; Length 1022;
Best Local Similarity 49.6%; Pred. No. 0.00016;
Matches 126; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

QY 316 GCAATTACCCAGCTTGCCCAACGACGCTGCTTCCGTTATCGGGCGTATGAGTTGAC 375
DB 526 GCAACATTCTGCTGGCTCAACCACTCTGAGAAATGCTTAGGGACACAGACCTTGTC 585
QY 376 AAAAGCTTGAAGAACGCGACGAATCAACGTAACCGTCTCCGCCCTCGATGAAGCC 435
DB 586 CAGATCTTAGCTGACGAGAAAGATCGCCATCACTCCAGACTTTACTTGATATATCC 645
QY 436 GCCGGGCTTGGGGTGTGAAAGTCTCCTCGTTACGAATCAAGATTTGGTCCGCGAA 495
DB 646 ACCGACCTGTGGGGATCCGGTGGCCCGAGTGAATCAAGATTCGATTCGGTG 705
QY 496 GAAATCTTCCGCGAATGACGACAAATTACCGCGAAACGCGCCCGTATT 555
DB 706 CAGTTGACAGATCCATGCGACCGAGGCTGAGGCCACCCGGGAGCGAGCCAAAGTTC 765
QY 556 GCCGAATCCGAAG 569
DB 766 CTGCGAGCTGAAG 779

RESULT 37

US-09-252-991A-6989
Sequence 6989, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 6989
LENGTH: 1602
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6989

Query Match 4.5%; Score 42.4; DB 4; Length 1602;
Best Local Similarity 46.8%; Pred. No. 0.0022;
Matches 133; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

QY 439 GGGGCTTGGGGTGTGAAAGTCTCCTTACGAATCAAGATTTGTTCCGCCGCAAGAA 498
DB 1165 GCGACCTACGGGGTCAAGGTGTGAGGTGCGATCGACGCTGACCCCTCCCAAGGTG 1224
QY 499 ATCTTGGCGCAATGACGACCAATTAACGCCGCAAGCGGAAAAACGGCCCGATTGGC 558
DB 1225 ACCCTGGCGCACCGTGAACCGCATGCGCCGAGGCGGAGACCAATCGCACCGAGCGT 1284

QY 559 GAATCCGAGCGCTTAATAATCGAACAATCAACTTCCAGTGTGAGGCTGAAGCCGA 618
| | | | |
DB 1285 ACCGCGGAGCGCGTCCGAGGCTGCGAGATCCGTTCCGCGCGGAGCGCGCCGG 1344
QY 619 ATCCAAATCCGAGGCGGAGGCTGAGGCTGAGGCTCAATGCGGCAATGCCGAGAAATC 678
| | | | |
DB 1345 GTGATCCAGGCGGAGGCTTCCGTGAAAGCCGCGAATGAGGCCCGAGCGGCTCGAG 1404
QY 679 GCCCGCATCAACCGCGCAAGGCGGAAATCCCTGCGCCT 722
| | | | |
DB 1405 GCGGCGCATCTAAGCGCAAGGCTACGCGGTTCCCGGAGCT 1448

RESULT 38
US-09-252-991A-7042
; Sequence 7042, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7042
; LENGTH: 2187
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7042

Query Match 4.5%; Score 42.4; DB 4; Length 2187;
Best Local Similarity 46.8%; Pred. No. 0.025;
Matches 133; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

QY 439 GGGGCTTGGGGGTGGAAGCTCCGTTACGAATCAAGATTGTTCCGCGCAAGAA 498
| | | | |
DB 92 GCGACCTACGCGGTCAAGTGTGCAAGTGGCATGCGACCTGACCTGCCAAGT 151
QY 499 ATCTTTCGCGCAATGCGCAAAATTCGCGCAAGCGCAAAAGCGCCGCTATTGCC 558
| | | | |
DB 152 ACCCTCGCGCCACCGTCGACCGCATGCGCGGAGCGGAGCAATCGCACGAGCT 211
QY 559 GAATCCGAGGCGGTAAATCGAACAATCAACTTCCAGTGTGAGGCTGAAGCCGA 618
| | | | |
DB 212 ACCGCGAGGCGCGTCCGAGGCTGCGAGATCCGTTCCGCGCGGAGCGCGCCGG 271
QY 619 ATCCAAATCCGAGGCGGAGGCTGAGGCTGAGGCTCAATGCGGAGAAATC 678
| | | | |
DB 272 GTATCCAGGCGGAGGCTTCCGTGAAAGCCGCGAATGAGGCCCGAGCGGCTCGAG 331
QY 679 GCCCGCATCAACCGCGCAAGGCGGAAATCCCTGCGCCT 722
| | | | |
DB 332 GCGGCGCATCTAAGCGCAAGGCTACGCGGTTCCCGGAGCT 375

RESULT 39
US-09-221-017B-544
; Sequence 544, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
; APPLICANT: Rose, Bruce C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto

QY 626 AATCCGAGGCGAGGCTGAGGCTGCGTCAATGCTCAATGCCGAGAAATCGCCGA 685
| | | | |
DB 5 AATCGAGGCTGAAGTGAAGTCAAGTCCATCAACAGCTGAGGAGGAGGAGCGCAAG 64
QY 686 TCAACCGCGCCAAAGCGGAGGAAATCCCTGCGCTTGTGCGGAGCAATGCCGAG 745
| | | | |
DB 65 TTCTCAGAGCCAAAGCTGAGGCAAGGCTAAGATATTGTTGCTCAAGGAGCGGAG 124
QY 746 CCATCCGCAATTCGCGCGCG 767
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DB 125 CTATCCGCAAGTCAAGCGAAGC 146

STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
FILING DATE: 23-DEC-1998
APPLICATION NUMBER: US/09/221,017B
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 544:
SEQUENCE CHARACTERISTICS:
LENGTH: 503 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
ORGANISM: PORYPHYROMONAS GINGIVALIS
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1...503
US-09-221-017B-544

Query Match 4.3%; Score 41.2; DB 3; Length 503;
Best Local Similarity 55.6%; Pred. No. 0.03; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 63;

RESULT 40
US-08-181-271A-106
; Sequence 106, Application US/08181271A
; Patent No. 5614395
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.

APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Spertson, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Unnes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/181,271A
FILING DATE: 13-JAN-94
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/PI/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 1031 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-181-271A-106

Query Match 4.3%; Score 41; DB 1; Length 1031;
Best Local Similarity 48.1%; Pred. No. 0.047;
Matches 116; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

QY	365	TGAGTTGACAAACGTTTGAAGACGACGCAAAATCAAGTACCGTCTCCGCC	424
DB	390	TGAACCTGGACGATGTGTCAGCAGAAATGAATTCCTGTGGAAGAAGC	449
QY	425	TCGATGAAGCCGCGGGCTTGAGGATGAAAGTCTCCGTTACGAAATCAAGATTGG	484
DB	450	TAGACAAAGCCATGACCTGTTATGTACGAAATCCTTCAACCTTAATTACACTTG	509
QY	485	TTCCGCCGCAAGAAATCCTTCGCGCAATGCAGCACAATTAACCGCGACGCAAAAAC	544
DB	510	AGCTGATCAACAGATTAAACGTCCATGAACGAAATCAACGCCGCGCAGATGAGAG	569
QY	545	GCGCCCGATTATCCGAATCCGAAGCCGTAATCGAAATCAACCTTGCCAGTGGTC	604
DB	570	TGGCAGCGAGCAAAAGACAGAGGCTGAGAAATCATTCAGATCAAAAGACAGAGGTG	629
QY	605	A 605	
DB	630	A 630	

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Job time : 227 secs

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OM nucleic - nucleic search, using sw model

Run on: August 13, 2005, 23:21:02 ; Search time 754 Seconds
(without alignments)
8157.500 Million cell updates/sec

Title: US-10-018-470a-16

Perfect score: 948
Sequence: 1 atgaatttcattcattc.....gcagcaaacgcgaataa 948

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 7305758 seqs, 3244068913 residues

Total number of hits satisfying chosen parameters: 14611516

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Published Applications NA.*
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3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
23: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	174	18.4	1677	9	US-09-767-129-1
2	174	18.4	1720	20	US-10-425-115-95784
3	172	18.1	1296	9	US-09-738-626-1692
4	172	18.1	1426	21	US-10-494-675-5
5	172	18.1	3309400	9	US-09-738-626-1
6	169.8	17.9	948	15	US-10-156-761-6459
7	169.8	17.9	9025608	15	US-10-156-761-1

	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
	165	160.2	158.8	156	155.6	155.6	155.6	155.6	155.6	155.6	155.6	155.6	155.6	155.6	155.6	155.6	148.2	142.2	133	126.8	126.8	124.8	117	111.2	111.2	111.2	111.2	110.4	110.4	96.4	96.4	95.6	91.8	84.6	80.2	80.2	80.2	
	17.4	16.9	16.8	16.5	16.5	16.5	16.5	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	15.6	15.0	13.3	13.4	13.4	13.2	12.3	11.7	11.7	11.7	11.7	11.6	11.6	10.2	10.2	10.1	9.7	8.9	8.5	8.5	8.5	
	1930	1218	1621	1722	1888	1975	1303	1398	1842	1910	1914	1916	1916	1916	1916	1916	852	805	1123	727	732	742	1091	518	518	518	518	504	504	691	691	683	622	100848	948	454	454	454
	US-10-719-993-176	US-10-260-238-266	US-10-437-963-76664	US-10-424-599-80498	US-10-719-993-177	US-10-719-993-178	US-10-956-157-1850	US-10-956-157-1850	US-10-956-157-1850	US-10-956-157-1850	US-10-956-157-1850	US-10-956-157-1850	US-10-956-157-1850	US-10-956-157-1850	US-10-956-157-1850	US-10-956-157-1850	US-10-425-114-26660	US-10-425-115-13230	US-10-425-114-21145	US-10-437-963-76661	US-09-878-134-349	US-10-767-701-5816	US-10-425-114-19667	US-09-922-217-1031	US-09-833-263-1031	US-10-025-380-1031	US-09-998-598-841	US-09-998-598-841	US-10-198-846-13409	US-09-815-343-1428	US-10-097-105-1428	US-09-969-034-1476	US-09-998-598-1161	US-10-672-787-39	US-10-767-701-13154	US-09-878-178-193	US-10-046-935-193	US-10-146-502-193
	Sequence 176, App	Sequence 266, App	Sequence 76664, A	Sequence 80498, A	Sequence 177, App	Sequence 178, App	Sequence 1850, App	Sequence 7085, App	Sequence 1001, App	Sequence 24973, A	Sequence 12975, A	Sequence 37, App	Sequence 34, App	Sequence 34, App	Sequence 1, Appl	Sequence 1, Appl	Sequence 26660, A	Sequence 13230, A	Sequence 21145, A	Sequence 76661, A	Sequence 349, App	Sequence 5816, App	Sequence 19667, A	Sequence 1031, App	Sequence 1031, App	Sequence 1031, App	Sequence 841, App	Sequence 58, App	Sequence 13409, A	Sequence 1428, App	Sequence 3476, App	Sequence 1161, App	Sequence 39, App	Sequence 13154, A	Sequence 193, App	Sequence 193, App	Sequence 193, App	

ALIGNMENTS

RESULT 1
US-09-767-129-1
; Sequence 1, Application US/09767129
; Patent No. US20010005746A1
; GENERAL INFORMATION:
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Nadiampalli, Ramgopal
; TITLE OF INVENTION: Simmons, Carl R.
; TITLE OF INVENTION: Stomatin-Like Genes and Their Use in
; FILE REFERENCE: 5718-58
; CURRENT APPLICATION NUMBER: US/09/767,129
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 09/395,397
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1677
; TYPE: DNA
; ORGANISM: Zea mays
US-09-767-129-1

Query Match 18.4%; Score 174; DB 9; Length 1677;
Best Local Similarity 52.4%; Pred. No. 1e-47;
Matches 433; Conservative 0; Mismatches 360; Indels 33; Gaps 1;
60 CGTCATCCCGCCAGAGAGTCACCTGTCGAAAGCTCGGCGCTTCATCGCCCTT 119
337 CATAGTCCGAGAGAGAGCTTACTGTGGAGAGATTGGGAAGTATCTCAAGACCTT 396

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OY 120 GACGGCCGGTTTGAATATTTTATCCCTTATCGACCGCGCTACCGCATTCGCT 179
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 397 CGGCTCCGGGTTCCACCTCTGATCCCGCGCTCAACGGTATGGCTTAGTGCACTCCGT 456
OY 180 GAAGAAATCCCTTTAGACGTACCGACGAGTGTGATCAGCGCGATTAATACGAATT 239
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 457 CAAGAGAGAGACATCCCTATCCCTACACAGAACCCATCACAGAGCAACAGTCAACAT 516
OY 240 GACTTTGACGGCATCTATCTATTTCCAAAGTAAACGATCCCAAACCTCGCTCATACGGTTC 299
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 517 ACAGATTGACACGCTATCTATGTCAAGATCAATGAGACCTTACCTTGTCTTATGGTGT 576
OY 300 GAGCACTACATTTATGCAATTAACCGAGTTGCCCAACGACGCTGCTTCCGTTATGCT 359
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 577 GAGAAATCCATCTATCTGCTCTCAACTTGCAACAAACATGAGAAAGTAACTGG 636
OY 360 GCGTATGAGATTGACAAACCGTTTGAAGAACGACGCAATCAACAGTACCGTGTCTC 419
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DB 637 GAAGATTAACCTTAGATTAAGACTTTTGAAGAGAGATGATTAATGAGAAATTTGTAG 696
OY 420 CGCCCTCATGAAAGCCGCGGGGCTTGGGGTGTGAAAGTCCCTGCTTACGAAATGAAGA 479
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 697 TGCCATCAATGAAAGACGACGATTTGGGCTGAAAGTGTATCCGCTATGAGATCAGGA 756
OY 480 TTTGGTCCGCGCAAGAAATCCTTCCGCAATGACGACGCAAAATTAACCGCGAAGCGGA 539
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DB 757 CATTAATCTCTCAGACAGGATTTAGCAGGCTATGAGATGACGCTGAGGCGAAGAAAGAA 816
OY 540 AAAACGCGCCGCTATTTGCCGAATCCGAAGCCGCTAAATCGAAATCAATCAACTTTCAG 599
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 817 AAAACGCGCTCAATCTCTTGAAGTCAAGAGGATGAAC----- 854
OY 600 TGGTACGCGTGAAGCCGAATTCGAATCCGAAGCCGACGCTCAGGCTCGGTCAATGC 659
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DB 855 -----AGGCCCAATCTTTGAATCAAGAGGAAAGAAAGACTGCGCAATCTTGA 903
OY 660 GTCCAATGCCGGAAGAAATCGCCGATCAACCGCGCAAGGCGAAGGGAATCCCTGCG 719
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 904 ATCTGAAGAGAGTATGTTGATCTAGCAAAACCGTGTCCAAAGGTTGGGCTGAAGCAATTC 963
OY 720 CTTTGTGCCGAAGCAATGCCAAGCAATCCGTCAATTTGCCGCGCTTCAAAACCA 779
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 964 TGCCAAGTCAAGAGCTAGCTGCTGGAATGAGATTGGTTTCAGATGCGATGACAACTGA 1023
OY 780 AGGCGGGCGGATGCGGTCAATCTGAAGATTGCCGAACAAATCGTAGCCGCTTCAACAA 839
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1024 AGGCAGTGCAAGGCTGCTAGCTGAACCTTGCAAGACAAATACATCGAAGCATTTCTCAA 1083
OY 840 TCTTGCCAAAGAAAGCAATACGCTGATTATGCCGCCCAATGTTGCC 885
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DB 1084 TCTGGCACAAAGAACAAATACAAATGCTTCTTCAGATGATAGTGCC 1129

RESULT 2
US-10-425-115-95784
; Sequence 95784, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 95784
; LENGTH: 1720
; TYPE: DNA
; ORGANISM: Zea mays
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; FEATURE:
; OTHER INFORMATION: Clone ID: MET4577_1886C.1
US-10-425-115-95784
Query Match 18.4%; Score 174; DB 20; Length 1720;
Best Local Similarity 52.4%; Pred. No. 1e-67;
Matches 433; Conservative 0; Mismatches 360; Indels 33; Gaps 1;

OY 60 CGTCATCCCCCAGAGAGAAATCCAGTTGTGAAAGGCTGGGCGTTTCCATCCGCGCT 119
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DB 346 CATAGTCCGAGAGAAAGGCTTACGTTGTGAGAGATCGGAAAGTATCTCAAGACCT 405
OY 120 GACGCGGTTTGAATATTTTGAATTCCTTATTCAGCCGCGTGCCTACCGCATTCGCT 179
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 406 CGGCTCCGGGTTTCCACCTCTGATCCCGCGCTGACCGATGCTTACGCTACGCTGCT 465
OY 180 GAAGAAATCCCTTTAGACGTACCGACCGAGTGTGATCAGCGCGGAGTAATAGCAATT 239
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 466 CAAGAGAGAGACATCCCTATCCCTCACAGAAAGCATCACAGAGCAACAGTCAACAT 525
OY 240 GACTGTGACGGCATCTATTTTCCAAATTAACGATCCCAACTCCCTCATACGCTTC 299
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 526 ACAGATTGACAGCTCATCTATGTCMAAGATCATGAGACCCCTACCTTCTCTATGGTGT 585
OY 300 GAGCACTCAATTAATGCAATTAACCGCTTCCCAACGACGCTGCTTCTTATTCG 359
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 586 GAGAAATCAATCTATGCTGTCTTACAACTTGCAAAACCAACATGAGAAAGTAACTCG 645
OY 360 GCGTATGAGATTGACAAACAGTTTGAAGAACGGAAGAAATCAACAGTACCGTGTCTC 419
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DB 646 GAAGATTAACCTTAATTAAGACTTTTGAAGAGAGAGATTAATGAGAAATTTGTAG 705
OY 420 CGCCCTCATGAAAGCCGCGGGGCTTGGGGTGTGAAAGTCCCTGCTTACGAATCAAGA 479
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 706 TGCCATCAATGAAGACGACGACAGATTTGGGCTGTAAAGTATCCGCTATGAGATCAAGGA 765
OY 480 TTTGGTCCGCGCAAGAAATCCTTCCGCAATGACGACGCAAAATTAACCGCGAAGCGGA 539
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 766 CATTAATCTCTCAGCAGGATTTAGCAGGCTATGAGATGAGCTGAGGCGAAGAAAGAA 825
OY 540 AAAACGCGCCGCTATTTGCCGAATCCGAAGCCGCTAAATCGAAATCAATCAACTTTCAG 599
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 826 AAAACGCGCTCAATCTCTTGAAGTCAAGAGGATGAAC----- 863
OY 600 TGGTACGCGTGAAGCCGAATTCGAACATCCGAAGGCGCTCAGGCTCGGTCAATGC 659
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DB 864 -----AGGCCCAATCTTTGAATCAAGAGGAAAGAAAGTCCGATCTTGA 912
OY 660 GTCCAATGCCGGAAGAAATCGCCGATCAACCGCGCAAGGCGAAGCGAATCCCTGCG 719
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DB 913 ATCTGAAGAGAGCTATGTTGATCTAGCAAAACCGTGTCCAAAGGTTGGGCTGAAGCAATTC 972
OY 720 CTTTGTGCCGAAGCAATGCCAAGCAATCCGTCAATTTGCCGCGCTTCAAAACCA 779
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DB 973 TGCCAAGTCAAGAGCTAGCTGCTGGAATGAGATTGGTTTCAATGAGATGAGACAACTGA 1032
OY 780 AGGCGGGCGGATGCGGTCAATCTGAAGATTGCGAAACAAATACGTAGCCGCTTCAACAA 839
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DB 1033 AGGCAGTGCAAGGCTGCTAGCTGAACCTTGCAAGACAAATACATCGAAGCATTTCTCAA 1092
OY 840 TCTTGCCAAAGAAAGCAATACGCTGATTATGCCCGCCCAATGTTGCC 885
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DB 1093 TCTGGCACAAAGAACAAATACAAATGCTTCTTCAGATGATAGTGCC 1138

RESULT 3
US-09-738-626-1692
; Sequence 1692, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
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APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1998-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 1692
LENGTH: 1296
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
US-09-738-626-1692

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Query Match 18.1%; Score 172; DB 9; Length 1296;

Best Local Similarity 51.7%; Pred. No. 4.3e-47;

Matches 391; Conservative 0; Mismatches 365; Indels 0; Gaps 0;

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QY 12 CATTAATCTTGTGGAGCGCGTGGCTTTTCGGCTTCAATCTTGTGTCATCCCGCA 71
DB 21 CATTAATCTTGTGGAGCGCGTGGCTTTTCGGCTTCAATCTTGTGTCATCCCGCA 80
QY 72 GCAGAAAGTCACGTTGTGAAAGGCTCGGCGCTTTCATCGCGCCCTGACGCGCGTT 131
DB 81 GGGTGAAGCGCGCTGATGAAAGCTTGTGTAAGTACACCGGACCGTTTCAAGTGGCT 140
QY 132 GAATATTTGATTCCTTTATGACCGCGTGGCTTACCGCCATTCGCTGAAAGAAATCCC 191
DB 141 GACCGTGGTGGTTCATTCGTGACCGAGTACCGCGCAAGATGACACCGGTGAGCGCT 200
QY 192 TTTAAGACGACCGAGCGTGTGATCGCGCGCAATTAAGCAATGATGCTGTTGACGG 251
DB 201 GGTTCATTTCCACCGCGAGCGTGTATTAACCAAGCAACCTGACCGTGGCATGATAT 260
QY 252 CATCATCTATTTCAAGTAACGATCCCAACTCGGCTCATACGTTTCAGACAACTACAT 311
DB 261 CGTGTGACCTTTCGAATCAAGCAACGAGCGCGCATCTACGCGGTGAGCACTACAT 320
QY 312 TATGCAATTAACCGAGCTTCCCAACGACGCTGCGTTCGTTATCGGCGTATGAGATT 371
DB 321 CGTGTGATGAGCAAGATTTCTGTAGCAACTTTCAGAGCGTTGTGGTGGCATGACCT 380
QY 372 GGAAGAAAGCTTGAAGAAAGCGCAATCAAGTACCGTGTCTCCGCGCTCGATGA 431
DB 381 GGAAGAAAGCTTCACTTCAAGTACGTAATCAACCGCGCTCCGTTGCGAGCGTCAATC 440
QY 432 AGCGCGCGGCGCTTGGGCGTGAAGATCTCCGTTAAGAAATCAAGATTTGGTTCCGC 491
DB 441 AGCAACCAACCAATGAGGCGCTGCGCATCGCGTGTGAAGTAAAGCAATGATTCGCG 500
QY 492 GCAAGAAATCTTTCGCGCAATGAGCAACAAATTAACCGCGCAACGCGAAACGCGCGG 551
DB 501 ACCATCATCTCAAGCATGATGAGAAAGAGATGAAGGAGACCGTGAAGAAAGCGCGCAC 560
QY 552 TATTCGCAATTCGAGAGCGCTGTAATTCGAACAAATCAACTTTCGAGTGTCAAGGTGA 611
DB 561 CATTTTGAACCGCAAGAGTCAAGCGCAAGCGCAATCAAACTGCGAAGGTGAAAAAGCA 620
QY 612 AGCGAAATTCGAACCAATTCGAAGGCGAGGCTCAGGCTGCGGTAAGCGCTCAATTCGCA 671
DB 621 AGCGAAATTCGAACCAATTCGAAGGCGAGGCTGAGGTAAGCAACGATCATCTTGAACGCA 680

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QY 672 GAAATCCCGCATCAACCGCGCAAGCGCAAGCGCAATCTTGTGTCGCA 731
DB 681 AGCGCAAGCATGATCTTGGCGCGCGCAAGGTAAGCGCGACGAGTCACTTCAAGCGCA 740
QY 732 AGCGAATCCGAGCGCATCTTCAATTTGCGCGCG 767
DB 741 GGGTGAAGCGCGAGCATCAAAAGTCAACGCGACG 776

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RESULT 4

US-10-494-675-5

Sequence 5, Application US/10494675

Publication No. US20050019877A1

GENERAL INFORMATION:

APPLICANT: Zelder, Oskar

APPLICANT: Pompejus, Markus

APPLICANT: Schroder, Hartwig

APPLICANT: Krogger, Burkhard

APPLICANT: Klopptroge, Corinna

APPLICANT: Habermeyer, Gregor

TITLE OF INVENTION: Genes coding for metabolic pathway proteins

FILE REFERENCE: BG1-163US

CURRENT APPLICATION NUMBER: US/10/494,675

PRIOR FILING DATE: 2004-05-04

PRIOR APPLICATION NUMBER: PCT/EP02/12141

PRIOR FILING DATE: 2002-10-31

PRIOR APPLICATION NUMBER: DE 101 54 292.1

PRIOR FILING DATE: 2001-11-05

NUMBER OF SEQ ID NOS: 164

SEQ ID NO 5

LENGTH: 1426

TYPE: DNA

ORGANISM: Corynebacterium glutamicum

FEATURE:

NAME/KEY: CDS

LOCATION: (101)..(1396)

OTHER INFORMATION: RXA00152

US-10-494-675-5

Query Match 18.1%; Score 172; DB 21; Length 1426;

Best Local Similarity 51.7%; Pred. No. 4.5e-47;

Matches 391; Conservative 0; Mismatches 365; Indels 0; Gaps 0;

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QY 12 CATTAATCTTGTGGAGCGCGTGGCTTTTCGGCTTCAATCTTGTGTCATCCCGCA 71
DB 121 CATTAATCTTGTGGAGCGCGTGGCTTTTCGGCTTCAATCTTGTGTCATCCCGCA 180
QY 72 GCAGAAAGTCACGTTGTGAAAGGCTCGGCGCTTTCATCGCGCCCTGACGCGCGTT 131
DB 181 GGGTGAAGCGCGCTGATGAAAGCTTGTGTAAGTACACCGGACCGTTTCAAGTGGCT 240
QY 132 GAATATTTGATTCCTTTATGACCGCGTGGCTTACCGCCATTCGCTGAAAGAAATCCC 191
DB 241 GACCGTGGTGGTTCATTCGTGACCGAGTACCGCGAAGATGACACCGGTGAGCGCT 300
QY 192 TTTAAGACGACCGAGCGTGTGATCGCGCGCAATTAAGCAATGATGCTGTTGACGG 251
DB 301 GGTTCATTTCCACCGCGAGCGTGTATTAACCAAGCAACCTGACCGTGGCATGATAT 360
QY 252 CATCATCTATTTCAAGTAACGATCCCAACTCGGCTCATACGTTTCAGACAACTACAT 311
DB 361 CGTGTGACCTTTCGAATCAAGCAACGAGCGCGCATCTACGCGGTGAGCACTACAT 420
QY 312 TATGCAATTAACCGAGCTTCCCAACGACGCTGCGTTCGTTATCGGCGTATGAGATT 371
DB 421 CGTGTGATGAGCAAGATTTCTGTAGCAACTTTCAGAGCGTTGTGGTGGCATGACCT 480
QY 372 GGAAGAAAGCTTGAAGAAAGCGCAATCAAGTACCGTGTCTCCGCGCTCGATGA 431
DB 481 GGAAGAAAGCTTCACTTCAAGTACGTAATCAACCGCGCTCCGTTGCGAGCGTCAATC 540
QY 432 AGCGCGCGGCGCTTGGGCGTGAAGATCTCCGTTAAGAAATCAAGATTTGGTTCCGC 491

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Db 541 AGCAACCAACCAATGGGGCTGCGCATGACCGCTGTGAACTAAGCAATTGATCCGCC 600
Qy 492 GCAAGAAATTCCTTGGCGAATGAGCAAAATTATCCGCCGGAAGCGGAAACCGGCCG 551
Db 601 ACCATTCATTCAGCATGATGAGAAAGCATGAGGACGATCCCTGAAAGCGGCCAC 660
Qy 552 TATTGCCGAATCCGAGGCGCGTAAATGAACTCAACTTGGCACTGTGTCAGCGTGA 611
Db 661 CATTGTGACCGGAGAAAGGTACAGCGGAAAGCGGACATCAAACTGCCGAAAGGTGAAAGCA 720
Qy 612 AGCCGAATTCACCAATCCGAGGCGGAGGCTGAGCTGCGGTCAATGCGTCAATGCCGA 671
Db 721 AGCCGAATTCCTCCAGGCTGAGGCTGAAAGCAAGCATCTCACTGAAAGCAAGAGCA 780
Qy 672 GAAATGCGCGGCGATCAACCGCGGCAAGGCGGAGCGGAATCCGCGCTTGTGTCGGA 731
Db 781 AGCCGAAGGATGATCTGCGCGCGGAGGTGAAAGCGGACGACCTTCTCAGGCGCA 840
Qy 732 AGCCAATGCCGAGGCGATCCGTCGAATTGCGCGCCG 767
Db 841 GGGTGAAGCCGAGCATCCAAAAGTCAAGCGCAGC 876

RESULT 5
US-09-738-626-1/c

; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAMA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENO, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: *Corynebacterium glutamicum*
US-09-738-626-1

Query Match 18.1%; Score 172; DB 9; Length 3309400;
Best Local Similarity 51.7%; Pred. No. 2.4e-45;

Matches 391; Conservative 0; Mismatches 365; Indels 0; Gaps 0;

Qy 12 CATATCTGTGTGGAGCGCGTGGCTTTTCGGCTTCAATCTTGTGTCATCCGCCA 71
Db 1619596 CATAGTTTTCGCGCTTGTGTGCGGTGTGTATCAAGTCAATAGCCCTGATTCGCCA 1619537
Qy 72 GCAGGAAGTCCAGCTTGTGAAAAGCTGGGCGTTTCCATGCGCGCTGAGCGCGGTTT 131
Db 1619536 GGGTGAAGCCGCGCATTTGAAGCGCTTGTGTAGTACACCGCACCGTTTCAGGCGGCT 1619477
Qy 132 GAATATTTTGAATCCCTTATGACCGGCGCTTACCGCATTCGCTGAAAAGAAATCC 191
Db 1619476 GACCTGCTGTTTCATTCGTGAGACGATACCGCAAGATGACACCCGCTGAGCGGCT 1619417
Qy 192 TTAGACGTACCAAGCGGTCTGCATCAAGCGGCGATATATGCAATTGACTGTGACGG 251

Db 1619416 GGTCTCATTTCCACCGGAGGCTGTATTATCCCAAGACAACTGACCGGTGGCATGATAT 1619357
Qy 252 CATCATGATTTTCAAGTAACCATCCAACTGCGCTCATATGAGTTTGAGCACTACAT 311
Db 1619356 GTGTGTGACTTTCATAATCAAGCAAGACGCGCATCTTACGCGCTGAGCACTACAT 1619297
Qy 312 TATGCAATTTACCAAGCTTGGCCCAAGACGCTGCTGTTATCGGCGCTATGAGTT 371
Db 1619296 CGTGTGTGAGAGGATTTCTGTAGCAACTTGTGAGAGTTTGTGCGTATGACCT 1619237
Qy 372 GGAAGAAAGCTTTGAGAGAGCGGACGAATTAAGTACGTTCCGCTTCGCTGATGA 431
Db 1619236 GGAAGAAACCTCTCACTTCACTGACGTGATCAACCGCGCTCTGTCGCGAGCTGATGC 1619177
Qy 432 AGCGCGCGGCGCTTGGGCTGTGAAAGTCTCCGTTAAGAAATCAAGATTTGTTCGCC 491
Db 1619176 AGCAACCAACAAATGGGCGCTGCGCATGACCGGTGTGAACTAAGCAATTGATTCGCC 1619117
Qy 492 GCAAGAAATCCTTGGCGCATGAGCAAGCAAAATTAACCGCGCAAGCGGCGCG 551
Db 1619116 ACCATTCATTCAGCAATGATGAGAAAGCATGAGGCAAGACGCTGAAAAGCGCGCAC 1619057
Qy 552 TATTGCCGAATCCAGGCGCTAAATTCGAACAAATCACTTGCAGTGTGAGCTGA 611
Db 1619056 CATTTTGACCGCAGAGGTACGCGGCAAGCGGACATCAAACTCCGAAGGTGAAAAGCA 1618997
Qy 612 AGCCGAATTCGAATCCGAGGCGGAGGCTCAGGCTGCGTCAATGCTCAATGCGCA 671
Db 1618996 AGCCGAATTCCTCCAGGTGAGGCTGTGAAAGCAAGCATCTCACTTGAACGAGAAAGCA 1618937
Qy 672 GAAATGCGCGCGCATCAACCGCGCAAGGCGGAAGCGGAATCCCTGCGCTTGTGCGCA 731
Db 1618936 AGCCGAAGGATGATCTCGGCGCGGAGGAGGAAGCGGACGATACCTCCAGGCGCA 1618877
Qy 732 AGCCAATGCCAGGCGATCCGTCGAATTGCGCGCCG 767
Db 1618876 GGGTGAAGCCGAGCATCCAAAAGTCAAGCGCAGC 1618841

RESULT 6
US-10-156-761-6459

; Sequence 6459, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 6459
; LENGTH: 948
; TYPE: DNA
; ORGANISM: *Streptomyces avermitilis*
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(948)
US-10-156-761-6459

Query Match 17.9%; Score 169.8; DB 15; Length 948;
Best Local Similarity 53.6%; Pred. No. 2e-46;
Matches 354; Conservative 0; Mismatches 307; Indels 0; Gaps 0;

```

QY 11 TCATTATCTGTTGGCAGCCGCGGTTTGGCTTCAAACTCTTGTGTCATCCCC 70
DB 23 TGATCATCTGTGTGTGTGTGTCTTTCATCGCTGTATCAAGCAATCCAGCTCATCCGCG 82
QY 71 AGCAGAGATCCAGCTTGTGCAAGAGCTCGGCGCTTTCATCGCCCTGACGCGGTT 130
DB 83 AAGCAGGCGCGGCTTGTGCAAGAGCTCGGCGCTTTCATCGCCCTGACGCGGTT 142
QY 131 TGAATATTTTGAATTCCTTTATCGACCGCGTGCCTTACCGGCTTGTGAAAGAAATTC 190
DB 143 TGAATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 202
QY 191 CTTTAGAGTACCGCAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 250
DB 203 TCGTTCCTGTCTCCCGCGAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 262
QY 251 GCATCATCTATTTCCAGATTAACGATCCCAACCTGCGCTTATACGCTTGAAGCACTACA 310
DB 263 CGTATCATCTATTAACGATTAACGATCCCAACCTGCGCTTATACGCTTGAAGCACTACA 322
QY 311 TTATGCAATTAACGATTTGCGCAACGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 370
DB 323 TCCAGGCGATCGAGAGCTCACGCTCACGCTCGCAACATCATCGCGGCGATGAGAC 382
QY 371 TGGACAAACGTTTGAAGAGCGGACGAAATCAACATCGCTGTGTGTGTGTGTGTGTGTGTGT 430
DB 383 TGGACGCGACCTTCACTCCCGCGAGGATCAACGCGGCTGTGTGTGTGTGTGTGTGTGTGT 442
QY 431 AAGCGCGCGGCGCTTGGGGGTGTGAAGTCTCGTTACGAATTCAGAGATTTGGTTCCGC 490
DB 443 AAGCGCGCGGCGCTTGGGGGTGTGAAGTCTCGTTACGAATTCAGAGATTTGGTTCCGC 502
QY 491 CGCAAGAAATCTTGTGCGCAATGCAAGCAATTAACGCGCGAAGCGGAAACGCGCGC 550
DB 503 CGACCTTCATCGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 562
QY 551 GTATTGCCGAATCCGAAGCGCGTAAATGAAACAAATCACTTGTGCAAGTGTGCGG 610
DB 563 CGATCTCTCACTCCCGCGAGGCGCGCAAGCGCGCTTCTCACTCCCGCGAGGATGAGAAC 622
QY 611 AAGCGGAATCCGAATCCGAAGCGCGCTCAAGCTGCGGTGCAATGTGTCGAATGCCG 670
DB 623 AGTCCCAATCTGTGCGCGCAAGGTGAGGCGCAAGGCGCGGCTGTGCGCGCGAGGCGG 682
QY 671 A 671
DB 683 A 683

```

```

RESULT 7
US-10-156-761-1
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608

```

```

; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

```

```

Query Match 17.9%; Score 169.8; DB 15; Length 9025608;
Best Local Similarity 53.6%; Pred. No. 2,3e-44; Indels 0; Gaps 0;
Matches 354; Conservative 0; Mismatches 307;

```

```

QY 11 TCATTATCTGTTGGCAGCCGCGGTTTGGCTTCAAACTCTTGTGTCATCCCC 70
DB 7760965 TGATCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 7761024
QY 71 AGCAGAGATCCAGCTTGTGCAAGAGCTCGGCGCTTTCATCGCCCTGACGCGGTT 130
DB 7761025 AAGCAGGCGCGGCTTGTGCAAGAGCTCGGCGCTTTCATCGCCCTGACGCGGTT 7761084
QY 131 TGAATATTTTGAATTCCTTTATCGACCGCGTGCCTTACCGGCTTGTGAAAGAAATTC 190
DB 7761085 TGAATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 7761144
QY 191 CTTTAGAGTACCGCAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 250
DB 7761145 TCGTTCCTGTCTCCCGCGAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 7761204
QY 251 GCATCATCTATTTCCAGATTAACGATCCCAACCTGCGCTTATACGCTTGAAGCACTACA 310
DB 7761205 CGTATCATCTATTAACGATTAACGATCCCAACCTGCGCTTATACGCTTGAAGCACTACA 7761264
QY 311 TTATGCAATTAACGATTTGCGCAACGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 370
DB 7761265 TCCAGGCGATCGAGAGCTCACGCTCACGCTCGCAACATCATCGCGGCGATGAGAC 7761324
QY 371 TGGACAAACGTTTGAAGAGCGGACGAAATCAACATCGCTGTGTGTGTGTGTGTGTGTGTGT 430
DB 7761325 TGGAGCGACCTTCACTCCCGCGAGGATCAACGCGGCTGTGTGTGTGTGTGTGTGTGT 7761384
QY 431 AAGCGCGCGGCGCTTGGGGGTGTGAAGTCTCGTTACGAATTCAGAGATTTGGTTCCGC 490
DB 7761385 AAGCGCGCGGCGCTTGGGGGTGTGAAGTCTCGTTACGAATTCAGAGATTTGGTTCCGC 7761444
QY 491 CGCAAGAAATCTTGTGCGCAATGCAAGCAATTAACGCGCGAAGCGGAAACGCGCGC 550
DB 7761445 CGACCTTCATCGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 7761504
QY 551 GTATTGCCGAATCCGAAGCGCGTAAATGAAACAAATCACTTGTGCAAGTGTGCGG 610
DB 7761505 CGATCTCTCACTCCCGCGAGGCGCGCAAGCGCGCTTCTCACTCCCGCGAGGATGAGAAC 7761564
QY 611 AAGCGGAATCCGAATCCGAAGCGCGCTCAAGCTGCGGTGCAATGTGTCGAATGCCG 670
DB 7761565 AGTCCCAATCTGTGCGCGCAAGGTGAGGCGCAAGGCGCGGCTGTGCGCGCGAGGCGG 7761624
QY 671 A 671
DB 7761625 A 7761625

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RESULT 8
US-10-719-993-176
; Sequence 176, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARBELL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/10/719,993
; PRIOR FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342

```

SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 176
 ; LENGTH: 1930
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-719-993-176

Query Match 17.4%; Score 165; DB 20; Length 1930;
 Best Local Similarity 50.2%; Pred. No. 1.3e-44;
 Matches 433; Conservative 3; Mismatches 418; Indels 9; Gaps 1;

```

QY 62 TCATCCCCAGAGAGTCCAGTGTGCGAAGGCTCGGCGTTTCCATGCGCCCTGA 121
DB 763 TCGRCGCGACGAGAGGCTGGGTGGTGGAGCAATGGCGATTCCACCGGATCCCTGG 822
QY 122 CGGCGGTTTAAATTTTGAATCCCTTATCGACCGGGTGCCATCCGCCATTGCGTGA 181
DB 823 AGCTGTGTTTGAACATCTCTATCCCTGTGTTAGACCGGATCCGATGTGACAGTCTCA 882
QY 182 AAGAAATCCCTTGAAGTACCCAGCCAGTCTGATCAGCGCGGATATACGCAATTGA 241
DB 883 AGGAAATGTATATCAAGTGTGCTGAGCAGTGGCTGTGACTCTGACAAATGTAATCTGCG 942
QY 242 CTGTGACGCGCATCATATTTCAGAGTACCGAATCCGAACTGCGCTCATACGGTTGCA 301
DB 943 AATTCGATGAGATCCTTAACTGCGCATCATGACCTTTACAGGCAAGCTACGGTGTGG 1002
QY 302 GCAACTACATTAATGCAATTAACCAAGTCCCAAGACGCTGCTTATCGGGC 361
DB 1003 AGGACCTGAGTATGCGCTACCCAGCTAGCTCAAAACAACATGATCAGAGCTCGGCA 1062
QY 362 GTATGAGTGTGACAAACGTTTGAAGAACGCAAGCAATCAAGTACGCTGCTTCGG 421
DB 1063 AACTCTCTGTGACAAAGTCTTCGGGAAACGGAGTCCCTGAATGCCAGATTGTGATG 1122
QY 422 CCCTCGATGAAGCGCGCGGGCTTGGGTGTGAAGTCTTCGTTACGAAATCAAGATT 481
DB 1123 CVATCAACCAAGCTGTGATGTGCGGTATCCGCTGCTCCGTTATGATGATCAAGATA 1182
QY 482 TGTGTTCCGCGCAAGAAATCTTTCGCGCAATGCGAGGCAAAATTAACGCCCGAAGCGG 538
DB 1183 TCCATGTGCCAACCCCGGTGAAGAGTGTATGCAAGATGACAGTGGGGCCAAAGAGGGT 1242
QY 539 -----AAAAAGCGCGCGTATGTCGCAATCCGAAGCGGTAAATCGAAATCAAAATCAACC 592
DB 1243 GGGAAAGAGGCTCAGGGCTCAGTGAAGGAGGAGGCGGAAAGCGGCCACAGTTCTAG 1302
QY 593 TTGCAAGTGTCAAGCGTGAAGCCGAAATCAACATCCGAAGCGGCTCAGGCTGCGG 652
DB 1303 AGTCTGAGGGAGACCGGAGATCGGCGATCAATGTGGCAGAAAGGAAAGAAACAGGCCCA 1362
QY 653 TCAATGCGTCCAAATGCGGAAAGAAATCGCGCGATCAACCGCGCCAAAGCGCAACCGGAAT 712
DB 1363 TCTGCGCTTCGGAAGCAAGAAAGGCTGAACAGATTAATCAAGCAGCAGAGAGGCGCAATG 1422
QY 713 CCCTGCGGCTTGTGGCGAGGCAATGCGGAAGCATCCGTCAATTGCGCGCGCCCTTC 772
DB 1423 CAGTTCTGCGGAGGCGCAAGGCTTAAGCTGAAGCTTAATTCGAATCCTGCTGAGCTCTGA 1482
QY 773 AAACCCAAAGCGGCGGATCGGTCAATCTGAAGATTGCGGAAACAATATCAATACCGCGGT 832
DB 1483 CACAACATTAATGAGATGACAGAGCTTCACTGACTGTGGCGGAGAGATATCAGCGGT 1542
QY 833 TCAACATCTTGGCCAAAGAAAGCAATACGCTGATTTATCCCGCAATGTTCGCGCATGCG 892
DB 1543 TCTCCAAATCGCGCAAGAGCTTCAACACTATCTACTGCTCTCAACCTGCGCGATGTCA 1602
QY 893 GCAGCTGATTTTGGCGCGCATG 915
DB 1603 CCAAGATGCTGCTCAGGCGCATG 1625

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RESULT 9

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US-10-260-238-266
; Sequence 266, Application US/10260238
; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicholas
; APPLICANT: Rieke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; PILE REFERENCE: 60111-NP
; CURRENT APPLICATION NUMBER: US/10/260,238
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO 266
; LENGTH: 1218
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-260-238-266

```

Query Match 16.9%; Score 160.2; DB 17; Length 1218;
 Best Local Similarity 53.4%; Pred. No. 4.3e-43;
 Matches 336; Conservative 0; Mismatches 233; Indels 0; Gaps 0;

```

QY 60 CGTCATCCCCAGAGAGTCCAGTGTGCGAAGGCTCGGCGTTTCCATGCGCGCCT 119
DB 258 CATGCCCGGAGAAAGAGGCTTGTGTGAGACGGTTCGGCAAGTACGTCAGAGCGCT 317
QY 120 GACGCGCGGTTGAATTTTGAATTCCTTTATGACCGGCTGCGCTACCGGCTTGGCT 179
DB 318 CGGCTCGGGAATCCAGTGTGCTGCTCCCTCTGTCGACCGCATGCTTACGTCACCTGCT 377
QY 318 GAAAGAAATCCCTTTAGACGTAACCCAGGCTGATCCGATCAATATGCAAT 239
DB 180 GAAAGAAATCCCTTTAGACGTAACCCAGGCTGATCCGATCAATATGCAAT 239
DB 378 CAGAGAGAGGCAATCCCGATCCCGACAGTCCGCGATCAACAGAGCAACGCTCCAT 437
QY 240 GACTGTGACGCGATCATTTATTTTCAAGTAAACGATCCCAATCGCTCATACGGTTC 299
DB 438 CCAGATCGAGCGGCTCTTACGTCAGATTTGATCCATCCTTCTCTATGATGT 497
QY 300 GAGCACTACATTAATGCAATTAACCGCTTGGCCAAACGAGCGTGGTCCGTATCGG 359
DB 498 GGAATATCCAAATTTTTCAGTATACAGCTTGCCTCAACAACTATGAGAACTGAGCTTGG 557
QY 360 GCGTATGAGATTTGCAAAAAGTTTGAAGAACGCGCAAGAAATCAACAGTACCGTCTC 419
DB 558 AAAGATTAACGTTAGCAAGACTTTTGAAGAGAGGATACACTAATTAAGCAAAATTTGAG 617
QY 420 CGCCCTGATGAGACCGCGCGGGCTTGGGTGTGAAGATCTCTCGTTACGAATCAAGGA 479
DB 618 GTCCATTATATGAGCTCACTGATTTGGGGAGCTGAATATGCTCGTTATGAGATCAAGGA 677
QY 480 TTGCTGCTCGCGCAAGAAATCTTCCGCGCAATGACAGGACAAATTAACCGCGGAACGGA 539
DB 678 TATATCTCCGCAACGCTGTGTTAAGTGTGCTATGAGATGCAAGCAGAGAGGAAGAA 737
QY 540 AAAAGCGGCGGTTATGCGCAATCGAAGCGGTTAAATCGAAACAATCAACTTTCAG 599
DB 738 AAAGCGTGCCTCAAAATCTTGAATCAGAAAGTGTGATGATGAGCAAAATCCGCGCAA 797
QY 600 TGTTCAGCGTGAACCGAAATCCAAATCCGAATCGAAGGCGCTCAGGCTGCGTCAATGC 659

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Db 798 GGGTGAAGCTGTAAGCAATTTCTTGCAAAAGTCTGAAGCAACTGCTGAGGAATTCAGATTGCT 857
Qy 660 GTCCAAATGCGGAAGAAATCGCCCGCATCA 688
Db 858 CTCTGAGGCCATGAGGACCAAGGCGACGA 886

RESULT 10
US-10-437-963-76664
Sequence 76664, Application US/10437963
Publication No. US2004012343A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 76664
LENGTH: 1621
TYPE: DNA
ORGANISM: *Oryza sativa*
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_76639C.1
US-10-437-963-76664

Query Match 16.9%; Score 160.2; DB 19; Length 1621;
Best Local Similarity 53.4%; Pred. No. 4.9e-43;
Matches 336; Conservative 0; Mismatches 293; Indels 0; Gaps 0;

Qy 60 CGTCATCCCGCCGAGGAGTCCAGTGTGCAAAAGGCTCGGAGCGTTTCATCGCGCCT 119
Db 258 CATCGTCCCGGAGGAGGCGTCTGTGTGAGGCGTTTCGCAAGTACGTAAGCGT 317
Qy 120 GACGCGCGGTTGAATATTTTGAATCCCTTTATCGACGCGTCCCTACCGCATTCGCT 179
Db 318 GCGGCTCCGAGTCCAGTCTGTCGTCGTCCTCGTCGACCGCATCGCTTACGTCACGCT 377
Qy 180 GAAAGAAATCCCTTTAGAGTACCGACGCGAGGTCTGCATCAGCGCGATTAATAGCAAT 239
Db 378 CAAAGAGAGGAGCCATCCCATCCCGACCAATCCCGCATCACCAAGAACAGTTCAT 437
Qy 240 GACTGTGAGCGGATCATATTTTCCAAATACCGATCCCAACTGCGCTCATACGCTTC 299
Db 438 CCAAGTCCGCGGCTCTTACGTCAGATTTGTATTTCTTACCTTCTCTTATGTGT 497
Qy 300 GAGCACTCATTTATGCAATTAACCAAGCTTGCCCAACAGCGCTGCTTCGTTATCG 359
Db 498 GAGAGATCAATTTTGGAGTCAATACAGCTTGCCCAACATATGAGAAAGTGG 557
Qy 360 GCGTATGAGTTGAGCAAAAGCTTTGAAGACCGCAAGAAATCAAGTACGCTCTC 419
Db 558 AAAGATTACGTAAGCACTTTTGAAGAGGAGATACATAAATGAGCAATTTGAG 617
Qy 420 CGCCCTCGATGAAGCGCGCGGCTTGAGGATGAAAGTCTCCGTTAAGAAATCAAGA 479
Db 618 GTTCATTAATGAGGCTGCAATGATTTGGGATGAAATGCTCTCTTATGAGATCGGA 677
Qy 480 TTTGTTCCGCGCAAGAAATCTTTCGCGCATGACGAGCAAAATTAACGCGCAACGCA 539
Db 678 TATATCTCGGCAAGGATGTTAAGGTGCTATGAGATGCAAGAGCAAGAAAGAA 737
Qy 540 AAAAGCGCGCGTATGCGGATTCGAAGCGCTAAATGCAAAATCAACTTTCGAG 599

Db 738 AAAGGTCCCAAAATCTTGAATCAGAAAGTGTATGTTGATCAGCAAAATCCGCAAA 797
Qy 600 TGTGACGCTGAAGCCCAATTCACAATTCGAAGGCGAGGCTCAGCTCGGCTAAATGC 659
Db 798 GGGTGAAGCTGTAAGCAATTTCTTGCAAAAGTCTGAAGCAACTGCTGAGGAATTCAGATTGCT 857
Qy 660 GTCCAAATGCGGAAGAAATCGCCCGCATCA 688
Db 858 CTCTGAGGCCATGAGGACCAAGGCGACGA 886

RESULT 11
US-10-424-599-80498
Sequence 80498, Application US/10424599
Publication No. US20040031072A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Soy Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 80498
LENGTH: 1722
TYPE: DNA
ORGANISM: *Glycine max*
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_43706C.1
US-10-424-599-80498

Query Match 16.8%; Score 158.8; DB 18; Length 1722;
Best Local Similarity 51.1%; Pred. No. 1.5e-42;
Matches 428; Conservative 0; Mismatches 377; Indels 33; Gaps 1;

Qy 65 TCCCCGAGGAGAGTCCAGTGTGCAAAAGGCTCGGCGTTTCCATCGCGCCTGACGG 124
Db 259 TCCCGAGAGAAAGCGTGTGTGATGAGCGATTCGGGAAGTACGTCAGACTCTTCCT 318
Qy 125 CCGGTTGAATTTTGAATCCCTTTATCGACCGGCGTCCCAACGCGCATTCGCTGAAG 184
Db 319 CCGGAATCAATTTTGAATTCCTTCTGTGATGAGTGTCTTATGCTATGCTGCTCAAG 378
Qy 185 AATCCCTTTAGACGTACCCAGCGTGTGATCAGCGCGCATTAATGCAATTGACTG 244
Db 379 AAGAGCTTATGATTTCCGACAGAGTGTATACCAAGACATGACCATCATCA 438
Qy 245 TTGACGGATCATTAATTTTCAAGTACCGATTCCAAACTGCGCTCATACGTTGAGCA 304
Db 439 TTGACGGGCTCTTATGTCAGATTTGATGATCTTAAGCTGCGCTTATGAGGATGAGA 498
Qy 305 ACTAATTAATGCAATTAACCGAGCTTGCCCAACAGCGTGGCTTCGTTATCGGCGTA 364
Db 499 ATCCATTTATCTGTGATTCGCTGCGGACAGACAAATGCTGAGCTTGTGA 558
Qy 365 TGAAGTTGCAAAAGCTTTGAAGACCGCAAGAAATCAACAGTACCGTCTCCGCC 424
Db 559 TTAATGCTGCAAGACCTTTGAGAAAGGACACACTCAATGAAGAAATGAGAGTCA 618
Qy 425 TCGATGAAGCGCGCGGCTTGAGGATGAAAGTCTCCGTTAAGAAATCAAGATTGG 484
Db 619 TTAATGCTGCAAGAAAGTGTGGGCTGAGTGTGCTTGAATGAAATGAGGATATCT 678
Qy 485 TTTCCGCGCAAAATCTTTCGCGCATGCAAGCAATTAACCGCGCAACGCAAAAC 544
Db 679 CTCTTCAAGTGAAGAGAGAGCATGATGAGATGACAGACAGAGCAAGAAAGAA 738
Qy 545 GCGCGGTATGCGGATTCGAAGCGCTTAATGCAAAATCAACTTTCGAGTGTCT 604
Db 739 GAGCTCAATTTCTGATGCTGAAGAGAAAGCAAGCTCAATTAACATTTGATGAA 798

Qy	605	AGCGTGAAGCCGAAATCAACAATTCCGAAGGGCAGAGCTCAGGCTGGGTCAATGGTGCA	664
Db	799	AGAAAGTTCACTGATCTTTAGCATAGA-----	827
Qy	665	ATGCCGAGAAAATGCSCCGCATCAACCGCGCCAAAGGCGAAGCGGAATCCCTGCCTTG	724
Db	828	--GCTGCAGAGATGGATCAAGTTAACAGACTCAAGGTGAGGCTGAAGCTATCTTGGCTA	885
Qy	725	TTCGCGAAGCCAATGCCGAGCGCATCCGTCMAATTGCCGCGCCCTTCAAACCBAAGCG	784
Db	886	AAGCAAAAGCAACGCTGAGGGACCTGCGCTGTTGTCTAAATCCCTTAAGAAATGGAG	945
Qy	785	GGGCGGATCGCGTCAATCTGAAGATTGGCGAACAATACTAGACCGCGTTCAACAATCTTG	844
Db	946	GACCTGAGGCAAGCAATTAAAGATTGCAGAGCAATATATTCAMCTTTCAGTAAACATAG	1008
Qy	845	CCAAAGAAAGCAATTCGCTGATTAATGCCCGCAATTTGGCCGACATCGGACGCTGAT	902
Db	1006	CCAAAGAGGCAACAATGTGTCTCTTAGCTGTGCATTCCAATCTGTGTAAACATGAT	1063

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RESULT 12
US-10-719-993-177
; Sequence 177, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 177
; LENGTH: 1888
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-177

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Query	March	16.5%	Pred. 156;	DB 20;	Length 1888;
Best Local Similarity	50.4%;	Pred. No. 1.4e-41;			
Matches 430;	Conservative	3;	Mismatches 381;	Indels 33;	Gaps 1
Dy	62	TCATCCCCAGCAGAGAGTCCACGTTGTGCAAAAGGCTCGGGCGTTTCATCGCGCCCTGA	121		
Db	763	TCGTGCCGACAGAGAGGCGCTGGGTGGTGGAGCGAATGGGGCGGATTCACCGGATCTCG	822		
Dy	122	CGGCGGGTTTGAAATATTTTGATTCCTCTTATGACCCGCGCTTACCGCCATTGGCTGA	181		
Db	823	AGCCGTGTTGAAACATCTCATCTCTGTGGTATGACCGGATCGAATGTGCGAGAGTCTCA	882		
Dy	182	AAGAAATCCCTTTAGACGTACCCAGCCAGGTCTGCATCAGCGCGCATATAAGCAATTGA	241		
Db	883	AGGAAATGTGTATCAACGTGCTGAGACAGTGGCGTGTACTCTCGACATGTAACTCTGC	942		
Dy	242	CTGTTGACGGCATCATCTATTTCCAGTACCGATCCCAACTCGCCTTCATACGGTTGGA	301		
Db	943	AAATCGATGAGAGTCTTTTACCTGCGGCATCATGAGACCTTTACAMGCGAAGCTACGGTGTGG	1002		
Dy	302	GCAATCATATATGCGCAATTCACGAGCTTGGCCAAACGAGGTGGGTTCCGTTATCGGGC	361		
Db	1003	AGGACCTTGAAGTATCCGTCACCCAGCTGACGTCAACAAACATGAGATCAGAGCTCGGCA	1062		
Dy	362	GTATGAGATTTGGACAAAAGTTTGAAGAAACGGACGAAATCAACAGTACCGTGTCTCG	421		
Db	1063	AACTCTCTGTGACAAAGTCTTCGGGGAAGGGGAGTCTCCCTGAATGCCAGCATTTGGAGT	1122		
Dy	422	CCCTCGATGAAGCCGCGCGGGCTTGGGGTGTGAAGATCTCTCGTTACGAATCAAGATT	481		
Db	1123	CAATCAACCAAGCTGCTGACTGTGCTGGGGGTATCCGCTGCTCTCGTTATGAGATCAAGATTA	1182		

QY	482	TGTTTCCGCCCCGGAAGAAATTCCTTGGCGCAATGCAAGCAACAATTTACCGCGCAACGGGAAA	541
Db	1183	TCATATGTGCACCCCGGGTGAAGAAGTCTATGCAATGTGCAAGTGGAGGACAGCCGGCGAA	124
QY	542	AACGCGCCGCTATTTGGCCGAATCCGAAGGCCGTMAAATCGAACAAATCAACTTGGCCAGTG	601
Db	1243	AACGGGCGACAGTTCTTAGAGTGTGA-----GG	126
QY	602	GTCAAGCTGGAAGCCGCAAAATCCACAACAATCCGAAGGCGAGGCTCAAGGTGGGGTCAATGCGT	661
Db	1270	GGACCCGAGAGTCGGCCCAATCATATGTGGAGAAAGGAGAAAGAGGCCAGATCTGGGCGCT	132
QY	662	CCAATGCGGAGAAATAATCGCCCGCATCAACCGGCGCAAAAGGCGCAAGCGGAGATCCCTGCGCC	721
Db	1330	CCGAAGCAGAAAGAAAGGCTGACACGATTAATACAGGACAGCAGAGAAAGGCGCAATGTGACGTTCTGG	138
QY	722	TTGTGTTCCGAAGCCCAATGCGCCGAGCCATCGTCAAAATTTGCGCGCGCGCTTCAAAACCCAG	781
Db	1380	CGAAGGCCCAAGGCTTAAGCTGAAAGCTTAATTCGATCTCTGGCTCAGGCTTGACACAACAATA	144
QY	782	GCGGGGCGGATGCGCGGTCAATCTGAAGATTGGCGGAAACAATAGCAGGCGGGTTCAACATC	841
Db	1450	ATGGAGATGCACGACCTTCACATGACTGTGGCGGAGCAGTATATCAAGCGGGTTCTCCAAAC	150
QY	842	TTGCGCAAGAAAGCAATACGCTGATTTATATGCCCCGCAATGTTGCCGACATCGGACGCTGA	901
Db	1510	TGGCCAAAGACTCGAACAATAATCTACTAGCCCTCCAAACCTTGCGGATGTGCACAGATG	156
QY	902	TTTCTGCGCGCATG	915
Db	1570	TGGCTCAGGCCCATG	1583

```

RESULT 13
US-10-719-993-178
; Sequence 178, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGLIL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178
; LENGTH: 1975
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-178

```

Query Match	16.5%	Score 156	DB 20	Length 1975
Beet Local Similarity	50.4%	Pred. No. 1.5e-41		
Matches 430	Conservative 3	Mismatches 388	Indels 33	Gaps 1
QY	TCATCCCCACAGAAAGTCCAGCTGTGCGAAAGGCTCGGGCGTTTCATCGCGCCCTGA	121		
DB	TCGTGCCACACAGGAGCGCTGGGTGGGAGCGCATGGGCGCATTCACCGGATCTCGG	822		
QY	CGGCGGTTGAATATTTTGAATCCCTTATTCGACCGCGTCCGCCATCCGCAATCGCTGA	181		
DB	AGCCGTGTTAAACATCTCATCTCTGTGTTAGACCGGATTCGATATGTGACAGACTTCA	882		
QY	182 AAGAAATCCCTTTAGACGTACCCAGCCAGGCTGTGCATCAGCGCGATTAATACGCAATTGA	241		
DB	883 AGGAATATGTATCAACGTGCTGAGCAGTGGGCTGTGACTCTGCACATTAATCTCTGC	942		
QY	242 CTGTTGACGGCATCATCTATTTCACAGTAACCGATCCCAACTGCGCTCATACGGTGTGA	301		
DB	943 AAATGTGAGAGTCCCTTTACCTGTGGACATCAGAACCTTTACAGGCAAGCTACGGGTGGG	1007		
QY	302 GCAACTCATTTATGGCAATTACCGACAGTTCGCCAAACGACGCTGCTTCGGTATCGGAG	361		

Db 1003 AGGACCCCTGAGTATGCCGTACCCAGCTAGCTCAAAACAACCATGATGATCAGAGCTCGGCA 1062

Qy 362 GTATGAGATTGGACAAAACGTTTGAAGACGCGACGAATCAACAGTACCGTCTCCG 421

Db 1063 AACTCTCTCTGGAACAAGTCTTCCGGGAAACGGGAGTCCCTGAATGCCAGCATTTGTGATG 1122

Qy 422 CCCCTGATGAAACCCCGCGGCGCTTGGGGTGTGAAGTCTCCGTTACGAATCAAGAT 481

Db 1123 CTAATCAACCAAGCTGTGACTGTGGGGTATCCGCTGCTCTCTGTTATGATCAAGATA 1182

Qy 482 TGTGTTCCGCGCCAGAAATCCTTGCGCGCAATGACGACAGCAAAATTACCGCCGAACGCAAA 541

Db 1183 TCCATGTGCCACCCCGGCTGAAGAAGTCTATGACAGTGTGAAGGCAAGGCGGCGGA 1242

Qy 542 AACGCGCCCGTATTGCGGATCCGAAGCGCTAAATTCAAACAATCAACTTGCACGTG 601

Db 1243 AACGGGCGACAGTTCTAGAGTCTGA-----GG 1269

Qy 602 GTCAAGCTGGAACCGGAATCCACAATCCGAAGCGAGGCTCAGGCTGCGGTCAATGCGT 661

Db 1270 GGAACCCGAGATCGCCCATCAATGTGCGAAGGGAAGAAAACAGGCCAGATCTTGCGCT 1329

Qy 662 CCAATGCGGAGAAATCGCCGCAATCAACCGCGCAAGGCGAAGCGGAATCCTTGCGCC 721

Db 1330 CCGAAGCGAAGAAAGGCTGAACAGTAAATCAAGGACGACGAGAGGCGCAGTCAATTTCTG 1389

Qy 722 TTGTTGCCGAAGCCAAATGCCAAGCCATCGGTCAATTTGCCGCGCCCTTCAAAACCAAG 781

Db 1390 CGAAGGCGCAAGGCTTAAGCTGAAGCTATTGCAATCTGCTGACGCTGACACAAACATA 1449

Qy 782 GCGGGGCGGATGCGGTCAATCTGAAGATTGGGGAACAATAGTGCGCGCTTCAACATC 841

Db 1450 ATGAGATGACGACAGCTTCACTGACTGTGCGCGAGCACTAATRTACGCGGTTCTCAAC 1509

Qy 842 TTGCCAAGAAGCAATACGCTGATTATGCCCGCAATGTTGGCGACATCGGACGCTGA 901

Db 1510 TGCGCAAGGATCTCCAAACATATCTTACTGCGCTCAACCCCTGGGAGTGTACACAGCANTG 1569

Qy 902 TTTCTGCCGGCATG 915

Db 1570 TGCGTCAAGGCATG 1583

RESULT 14

US-10-956-157-1850

; Sequence 1850, Application US/10956157

; Publication No. US20050118625A1

; GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Mounts, William

TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

FILE REFERENCE: 031896-043000 (AM 101081)

CURRENT APPLICATION NUMBER: US/10/956,157

CURRENT FILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 318605

SOFTWARE: PatentIn version 3.2

SEQ ID NO 1850

LENGTH: 1303

TYPE: DNA

ORGANISM: Homo sapiens

US-10-956-157-1850

	Query Match	Similarity	16.4%	Score 155.6	DB 21	Length 1303
	Best Local	Similarity	50.6%	Pred. No. 1.6e-41		
	Matches	432	Conservative	0	Mismatches 389	Indels 33; Gaps 1
Qy	62	TTATCCCCAGAGAGATGTCACAGCTTTCGAAAGCTGGGGGTTTCATCGCGCCGGA	121			
Db	182	TGTGTCCGAGCAGAGAGGCTCGGTGTGTGTGAGACCGAATGGCGCGATTCACCGAATCTGG	241			
Qy	122	CGCGCGGTTGAATATTTTGAATCCCTTATTCAGACCGCGTCGCTTACCGCATTCGCTGA	181			

Db	242	AGCGTGGTTGAACATCCCTCATCCCTGCTGTGTAGACCGGATCCGATATGTGTCAGAGTCTCA	301
QY	182	AAGAAATCCCTTTAAGCTGATCCCAAGCCAGGCTGCATGCAACGGCGGATATATAGCAATTTGA	241
Db	302	AGGAATATGTCAATCAACGTCGCTGAGCAGTCCGCTGTGCTCTCTCGCAAAATGTATCTCTGC	361
QY	242	CTGTTGACGGGCAATCATCTATATTTCCAAATTAACGATGCCAAATCTGCGCTCATACGTTTCGA	301
Db	362	AAATGATGTGAGTCTCTTTAAGCTGCGCATATGGAACCTTTACAAAGGCAAGCTACGCTGTGG	421
QY	302	GCAACTACATTTATGTGCAATTAACCAAGCTTGCACCAACGACGCTGCTCTGTTATCGGGC	361
Db	422	AGGACCCCTGAATATCCCGTCAACCCAGCTAGCTCAACCAACATAGATCAGAGCTCGGCA	481
QY	362	GTAATGAGTTGGACAAAAGTTTGAAAGACGGACGAATTCACAGTACCGTCTCTCCG	421
Db	482	AACTCTCTGTGGACAAAGCTTTCGCGGAAACGGGAGTCCCTGAAATGCAACATTTGTGATG	541
QY	422	CCCTGATGGAAGCCGCCCGGGGCTTTGGGGGTGTAAGTCCCTCGTTACGAATCAAGATTT	481
Db	542	CCATCAACCAACCTCTGATCTGTGGGTATTCGCTGCTCTCGTTATGAGATCAAGATATA	601
QY	482	TGTTTCGCGCGGAGAAATCTTGGCGCAATGACGAGCAAAATTACCGCGGAACGGGAAA	541
Db	602	TTCATGTGCAACCCCGGGTGAAAGAGTCTATGCAATGCAATGTGAGGACGAGCGCGGA	661
QY	542	AACGCGCCGTATTTCGCCAATCCGAAGCCCGTAAATCGAACAAATCAACTTGTCCAGTG	601
Db	662	AACGGGCCCAAGTTTGAAGTCTGA-----GG	688
QY	602	GTCAAGCTGGAAGCCGAATTCACAATTCGGAAGCGAGGCTCAGGCTGCGGTCAATGCGT	661
Db	689	GGACCCGAGAGTCGCGCATCAATGTGGCAGAAAGGGAAGAAACAGGCCCAATCTTGCCCT	748
QY	662	CCAATGCGAGAAATTCGCGCGCATCAACGCGCGCAAAAGCGGAATGCCCTGCGCC	721
Db	749	CCGAAGCAGAAAAGGCTGAACAGATTAATCAGGACAGAGAGGCCAGTGCAGTTCTGG	801
QY	722	TTGTTGCCGAAGCCATGCGCGAAGCCATCCGTCAATTGCGCGCGCTTCAAAACCCAG	781
Db	809	CGAAGGCCAAGGCTTAAGCTGAAGCATTTGCAATCTGCGTGAAGCTGTGACCAACATA	861
QY	782	GGGGGGCGGATCGGCTCAATCTGAAGATTGGGGAACATATCGTAGCGCGCTTCAACATC	841
Db	869	ATGAGAGATGCACAGCTTCACTGACTGTGGCGCAGATATGTCAAGGCGCTTTCCAAC	928
QY	842	TTGCCAAGAAAGCAATACGCTGATTTATGCCCGCCCAATGTGCCGACATGGGAGCGCTGA	901
Db	929	TGGCCAAAGATCCCAACACTATCTTACCTGCGCTCCAAACCTGGCGAATGTCAACGACATGG	988
QY	902	TTTCTGCGCGCAGT	915
Db	989	TGGCTGAGGCAATG	1002

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RESULT 15
US-10-956-157-7085
; Sequence 7085, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7085
; LENGTH: 1303
; TYPE: DNA

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ORGANISM: Homo sapiens
US-10-956-157-7085

Query Match 16.4%; Score 155.6; DB 21; Length 1303;

Best Local Similarity 50.6%; Pred. No. 1.6e-41;
Matches 432; Conservative 0; Mismatches 389; Indels 33; Gaps 1;

62 TCATCCCCCAGAGAGTCCAGTGTGCGAAAGGCTCGGGGCTTTCATCGCCCTGA 121
182 TCGTCCCGCAGAGAGGCTGGGTGGTGGAGCGAATGGCCGATTCACCGGATCTCG 241
122 CGGCGGTTTGAATTTTGAATCCCTTATCGACCGCGTGGCTTACCGCATTCGCTGA 181
242 AGCTGGTTGAACCTCTCATCCCTGTGTAGACCGATCGAATGTGAGAGTCTCA 301
182 AAGAAATCCCTTATGACCTACCGACCGCTGTGATCAACCGCGATATACGCAATGA 241
302 AGGAAATGTGATCAACGTGCTGAGCAGTGGCTGTGACTCTGCAATGTAACTGTG 361
242 CTGTTGACGGCATCTATTTTCAAGTAACCGATCCCAACTCGCTCATACGGTTGCA 301
362 AAATGATGAGATCTTTTACCTGGCATATGAGACCTTACAGGCAAGCTACGGTGG 421
302 GCAATCATATTATGCAATTACCGAGCTTGGCCAAAGCAGCGCTGCTTATCGGAC 361
422 AGGACCTGAGTATGCGTCAACCGAGCTCAAAACATGATGATCAGAGCTCGGCA 481
362 GTATGAGATTGAGCAAAACGTTTGAAGAACGAGCAAGAAATCAACGATACGCTCG 421
482 AACTCTCTGTGACAAAGTCTTCCGGAAAGGAGTCCCTGAAATCCGCAATTTGGATG 541
422 CCTGTGATGAAGCCCGGGGCTTGGGGTGTGAAGTCTCTCGTTACGAAATCAAGATT 481
542 CCATCAACCAAGCTGCTATGCTGGGTATCCGGTATCCGTTATGATGATCAAGATA 601
482 TGGTTCGCGCGAAGAAATCTTCCGCGATGCAAGCAAAATTAACCGCGAAGCGGAA 541
602 TCATATGTCCACCCCGGGTGAAGAGATCTATGCAATGACAGTGGAGGCGGCGGA 661
542 AACCGCGCGGATTTGGCCGAATCCGAAGGCCGTAATGAAACAAATCAACCTTGCATG 601
662 AACGGGCCACAGTTCTAGATCTGA-----GG 688
602 GTACGCGTGAAGCCGAAATCCCAATCCGAAGCGAGGCTCAGGCTCGGTCATGCGT 661
689 GGACCCGAGAGTGGCCATCAATGTGGCAAGAGGAAAGAAACAGGCCCAATCTGGGCT 748
662 CCAATGCGAGAAATGCGCCGCGATCAACCGCGCAAGCGGAGCGGAATTCCTGCGCC 721
749 CCGAAGCAGAAAGGCTGAACGATTAATCAAGGCGAGAGAGGCGAGTCAATCTGG 808
722 TTGTTTGGCGAAGCCATGCCAAGCATCCGTCAAATTTGCCCGGCTTCAACCCGAG 781
809 CGAAGGCCAAGGCTTAAGCTGAAGCTATTCGAATCTGCTGCACTTGAACAACTA 868
782 GCGGGCGGATGCGGTCATCTGAAGATTGCGGAACAATAGTAGCCGCTTCAACAATC 841
869 ATGAGATGCAAGCACTTCACTGAGTGTGGCGGAGCAATATGTCAAGCGCTTCTCAAC 928
842 TTGCGCAAGAAAGCAATACGCTGATTTATCCCGCAATGTTGCGCAATCGGAGCTGA 901
929 TGGCCCAAGGACTCCAACTATCTACTGCTCCAAACCTGGCGATGTCAACAGCATGG 988
902 TTTTGGCGCGCATG 915
989 TGGCTCAGGCGCATG 1002

RESULT 16
US-10-276-774-1001/c
; Sequence 1001, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 1001
; LENGTH: 1398
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-774-1001

Query Match 16.4%; Score 155.6; DB 18; Length 1398;

Best Local Similarity 50.6%; Pred. No. 1.7e-41;
Matches 432; Conservative 0; Mismatches 389; Indels 33; Gaps 1;

62 TCATCCCCCAGAGAGTCCAGTGTGCGAAAGGCTCGGGGCTTTCATCGCCCTCGA 121
1212 TCGTCCCGCAGAGAGGCTGGGTGGTGGAGCGAATGGCCGATTCACCGGATCTCG 1153
122 CGGCGGTTTGAATTTTGAATCCCTTATCGACCGCGTGGCTTACCGCATTCGCTGA 181
1152 AGCTGGTTTGAACCTCTCATCCCTGTGTAGACCGGATCCGATATGTGAGAGTCTCA 1093
182 AAGAAATCCCTTATGACGTACCGACCGAGTCTGATCAACCGCGATATACGCAATTGA 241
1092 AGGAAATGTGATCAACGTGCTGAGCAGTGGCTGTGACTCTGCAATGTAACTGTGC 1033
242 CTGTTGACGCAATATCTTATTCGAATACCGATCCCAACTGGCTTCAACGCTTCA 301
1032 AAATGATGAGTCTTTTACCTGGCATGAGCCCTTACAGGCAAGACTGAGTGG 973
302 GCACTACATATTATGCAATTAACCGAGCTTGGCCAAAGCAGCTGCTTCTGTATCGGAC 361
972 AGGACCTGAGTATGCGGTACCCAGCTCAGGCTCAAAACATGATGATGAGAGTCTG 913
362 GTATGAGTTGAGCAAAATCGTTTGAAGAACGCGAGCAAAATCAACAGTACGCTCTCCG 421
912 AACTCTCTGTGACAAAGTCTTCCGGGAACGGAGTCCCTGAATGCCAGCATTTGTGATG 853
422 CCTGTGATGAAGCCCGGGGCTTGGGTGTGAAGTCTTCCGTTTGAATCAAGATT 481
852 CCATCAACCAAGCTGCTGATGCTGGGTATCCGCTGCTTCCGTTATGATCAAGATA 793
482 TGGTTCGCGCGCAAGAAATCCTTGGCGAATGACGAGCAAAATTAACCGCGAAGCGGAA 541
792 TCATATGTCCACCCCGGGTGAAGAGTCTATGCAATGCAAGTGAAGGAGGCGGGA 733
542 AACCGCGCGGATTTGGCGAATCCGAAGGCCGTAATGAAACAAATCAACCTTGCAGTG 601
732 AACGGGCCACAGTTCTAGATCTGA-----GG 706
602 GTACGCGTGAAGCCGAAATCCCAATCCGAAGCGAGGCTCAGGCTGCGTCAATGCGT 661
705 GGAACCGAGAGTCCGCAATCAATGTGCAAGAGGAAAGGAAACAGGCCCAAGATCTGGGCT 646
662 CCAATGCGAGAAATGCGCCGCGATCAACCGCGCAAGGCGAAGCGGAATCCCTGCGCC 721
645 CCGAAGCAGAAAGGCTGAGACAGTAAATCAAGGAGAGAGGCCAGTGTCTGAG 586
722 TTGTTGCGAAGCCCAATGCGAAGCCATCCGTCAAATTTGCCCGCTTCAAAACCAAG 781
585 CGAAGGCCAAGGCTTAAAGCTGAAGCTATTCGATCTGTGCTGCACTGACAAACATA 526
782 GCGGGCGGATGCGGTCATCTGAAGATTGGGAAACAATAGTAGCGCGCTTCAACAATC 841
525 ATGAGATGCAAGCTTCACTGACTGTGGCCGAGAGTATGTAGAGCGCTTCTCAAC 466

QY 842 TTGCCAAGAAAGCAATACGCTGATTATGCCCCCAATGTTCCGACATGCGACCTCGA 901
DB 465 TGGCCAGAGACTCCAACTATCTACTGCTCCCAACCTGGCGATGTCACAGCATG 406
QY 902 TTTCTGCGCGCATG 915
DB 405 TGGCTCAGGCGCATG 392

RESULT 17
US-10-357-930-24973

Sequence 24973, Application US/10357930
Publication No. US20040259086A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
FILE REFERENCE: MRI-007BCN
CURRENT APPLICATION NUMBER: US/10/357,930
PRIOR FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 09/785,276
PRIOR FILING DATE: 2003-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24973
LENGTH: 1842
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: misc feature
LOCATION: 1841_1842
OTHER INFORMATION: n = A,T,C or G
US-10-357-930-24973

Query Match 16.4%; Score 155.6; DB 20; Length 1842;
Best Local Similarity 50.6%; Pred. No. 1.9e-41;
Matches 432; Conservative 0; Mismatches 389; Indels 33; Gaps 1;

QY 62 TCATCCCGCAGAGAAATGTCAGTGTGGAAGGCTCGGCGCTTTCATCGGCCCTCGA 121
DB 661 TCGTCGCGCAGAGAGGCGCTGGTGTGAGAGCAATGCGCATTCACCGCATCTCG 720
QY 122 CGCGCGCTTGAATATTTGATTCCTTATGACGCGCTGCGCTACCGCATTTGCTGA 181
DB 721 ACCCTGTTGAACCTCTATCTGTTTGAACCGGATCGGATGTCAGAGTCTCA 780
QY 182 AAGAAATCCCTTGAAGTACCGCAGGCTGTCATCAAGCGGATTAATACCAATGA 241
DB 781 AGGAATTTGTCAACAGCGTCCGAGCAGTCCGCTGTGATCTCGACAAATGTAACCTCG 840
QY 242 CTGTTGACGCGCATCTATTTTCAAGTAAACGATCCAAACTCGCTCATAGGTTCA 301
DB 841 AATCATGAGAGCTCTTACTGCGCATATGAGACCTTAAAGGCAAGCTACGCTGTG 900
QY 302 GCAACTACATTAATGCAATTAACGAGCTTGGCCAAAGCAGCGGCTTCGTTATGCGG 361
DB 901 AGGACCTGATGCTGCTGACCCAGACTAGCTCAAAACATGAGATCAAGACTCGGCA 960

QY 362 GTATGAGTTGAGCAAAAGTTTGAAGAGCGAGCAATCAACAGTACCGTCTCCG 421
DB 961 AACTCTCTGTGACAAATCTTTCGGGAACGGAGTCCCTGAATCCAGATTTGATG 1020
QY 422 CCTGTGATGAAGCCCGCGGCTTGGGTTGTAAGTCTCTCGTTACGAATCAAGATT 481
DB 1021 CCATCAACCAAGCTGTACTGTGGGTATTCGGCTCTCGTTATGATCAAGATTA 1080
QY 482 TGGTCCCGCCGAGAAATCTTGGCGCATGACGAGCAAAATTAACCGCCGAACGAAA 541
DB 1081 TCCATGTCCACCCCGGTGAAGAGTCTATGCAATGAGGTGAGGACAGCGCGGA 1140
QY 542 AACGCGCCGTTATTCGCAATCCGAAGCCGTTAAATGAAACAATCAACTGCGAGT 601
DB 1141 AACGGGCAACAGTTTGAAGTCTGA-----GG 1167
QY 602 GTACGCTGTAAGCCGAATTCGAACAATCCGAAGCGAGCTCAGCTCGTCAATGAGT 661
DB 1168 GGAACCCGAGAGTCCGCTCATATGTGCGAAGAGGAGAAACAGGCCAGATCTGGCT 1227
QY 662 CCAATGCCGAGAAATGCGCCGATCAACCGGCCAAAGCGAAGCGAATCTGCGCC 721
DB 1228 CGAAGCGAAGAAAGCTGAACAGATTAATCAGGCGAGAGAGCCAGTGCAGTTCTG 1287
QY 722 TTGTTCCGGAAGCCATGCGCAAGCCATCCGTCAAATTGCGCGCCCTTCAACCCA 781
DB 1288 CGAAGCGAAGCTGAAGCTGAAGTATTCGAATCTGCTGACCTGACACAACTA 1347
QY 782 GCGGGCGAGATGCGTCAATCTGAATGCGGAACAATACGTACCGCTTCAACAATC 841
DB 1348 ATGAGATGACAGACTTCACTGACTGTGCGGACAGATATGTCAGCGGTTCTCAAC 1407
QY 842 TTGCCAAGAAAGCAATACGCTGATTATGCCCCCAATGTTCCGACATGCGACCTCGA 901
DB 1408 TGGCCAGAGACTCCAACTATCTACTGCTCCCAACCTGGCGATGTCACAGCATG 1467
QY 902 TTTCTGCGCGCATG 915
DB 1468 TGGCTCAGGCGCATG 1481

RESULT 18

US-10-198-846-12975

Sequence 12975, Application US/10198846
Publication No. US20030099974A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12975
LENGTH: 1910
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: misc feature
LOCATION: 1, 2, 1909, 1910
OTHER INFORMATION: n = A,T,C or G
US-10-198-846-12975

Query Match 16.4%; Score 155.6; DB 14; Length 1910;
Best Local Similarity 50.6%; Pred. No. 2e-41;

```
Matches 432; Conservative 0; Mismatches 389; Indels 33; Gaps 1;
QY TCATCCCCCAGAGAGTCCACGCTTTCGAAAGGCTGGGGGTTTCATGCGCCCTGA 121
Db TCGTCCCGCAGAGAGGCTGGGTGGAGCGAATGGCCGATTTCCACCGATCTGG 241
QY 122 CGGCGGTTTGAATATTTTGAATCCCTTTATCGACCGCGTGGCTTACCGCATTCGCTGA 181
Db AGCCGTGGTTGAATCTCTCATCTCTGTAGTACCGGATCGAATATGTGAGAGTCTCA 301
QY 182 AAGAAATCCCTTTAGAGTACCCAGCCAGGTCTGATCAACCGCATATATACGAATTGA 241
Db AGGAAATGTCAATCAACGTGCTGAGCAGTGGCTGTACTCTCAATGATTAATCTGTC 361
QY 242 CTGTGAGCGCATCATCTATTTTCAAGTAACGATCCCAACTGCTCATACGGTTGA 301
Db AAATGATGAGTCTTTTACTGCGCATATGAGACCTTTACAGGCAAGCTACGGTGG 421
QY 302 GCAACTACATTATGCAATTAACCCAGCTTGGCCCAACGACGCTGGCTTCCGTTATCGGGC 361
Db AGGACCCGAGATATGCGGTCAACCCAGCTAGCTCAAAACCATGATCAAGGCTCGGA 481
QY 362 GTATGAGTGTGACAAAACGTTTGAAGAAGCGACGAATCAACATTCCTCTCTCG 421
Db AACTCTCTGTGACAAAAGTCTTCCGGGAAACGGAGTCCCTGAAATGCGCATTTGGATG 541
QY 422 CCTGTGATGAAGCGCGCGGGCTTGGGGTGTGAAGTCTCTCGTTACGAATTCAGATG 481
Db CCATTAACCAAGCTGTCTGATGCTGGGTATTCCTGCTGCTGTTATGATCAAGATA 601
QY 482 TGGTTCCGCGCAAGAAATCTTTCGCGAATGACAGGCAAAATTAACCGCCGAACCGGAAA 541
Db TCATATGTCACACCCGGGTGAAGAAGTCTATGAGATGACAGGTGAGGACAGGCGCGGA 661
QY 602 AACCGCGCCGTATTTCCGCAATCCGAGGCGGTAAATGAAACAATCAACTTGGCAATG 601
Db AACCGGCCACAGTTCTTGAAGTCTGA-----GG 688
QY 662 GTACGCGTGAAGCGCAATTCGAATTCGAAGCGGAGGCTCAGGCTCGGTCATATGCGT 661
Db GGACCCGAGAGTCCGCTCATATGTCGAGAGAGGAGAAACAGGCCCAAGATCTGGGCT 748
QY 749 CGAAGCGAGAAAGGCTGAACAGATTAATCAAGGACGAGAGAGGCGAGTCAAGTTCGG 808
Db 722 TTGTTGCGGAAGCCATGCGCAAGCTCCGTCGAATTTGCCCGCCCTTCAAAACCGAAG 781
QY 809 CGAAGGCGAAGGCTTAAGCTGAAGCTATTCGAATCTGGCTGCACTTGAACAACTA 868
Db 782 GCGGGGGGATGCGGTCAATCTGAAGATTTGCGGAACATATAGCTAGCGGTTCAACATC 841
QY 869 ATGAGATGACAGACCTTCACTGATGTGGCGGACGATATGTACGCGGTTCTCCAAAC 928
Db 842 TTGCGCAAGAAAGCAATACGCTGATTTATCCCGCAATGTTGCCGACATTCGACGCTGA 901
QY 929 TGGCGCAAGAGCTCCAACTATCTCACTGCTCCAAACCTGGGAGATGTCACAGCATGG 988
QY 902 TTTCTGCGCGCATG 915
Db 989 TGGCTCAGGCGCATG 1002
```

RESULT 19

```
US-10-119-428-37
; Sequence 37, Application US/10119428
; Publication No. US2003016581A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Xu, Chongjun
; APPLICANT: Wehrman, Tom
```

```
APPLICANT: Ren, Feiyan
APPLICANT: Ma, Yunding
APPLICANT: Zhou, Ping
APPLICANT: Zhao, Qing A.
APPLICANT: Yang, Yonghong
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US2003016581A1el Nucleic Acids and
FILE REFERENCE: 789CIP2
CURRENT APPLICATION NUMBER: US/10/119, 428
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 09/596,193
PRIOR FILING DATE: 2000-06-17
PRIOR APPLICATION NUMBER: 09/574,454
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: 09/519,705
NUMBER OF SEQ ID NOS: 55
SOFTWARE: pf_fl_genes Version 1.0
SEQ ID NO 37
LENGTH: 9098
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (75) .. (9098)
US-10-119-428-37

Query Match 16.4%; Score 155.6; DB 16; Length 9098;
Best Local Similarity 50.6%; Pred. No. 4.4e-41;
Matches 432; Conservative 0; Mismatches 389; Indels 33; Gaps 1;
QY 62 TCATCCCCCAGAGAGTCCACGCTTTCGAAAGGCTGGGGGTTTCATGCGCCCTGA 121
Db TCGTCCCGCAGAGAGGCTGGGTGGAGCGAATGGCCGATTTCCACCGATCTGG 252
QY 122 CGGCGGTTTGAATATTTTGAATCCCTTTATCGACCGCGTGGCTTACCGCATTCGCTGA 181
Db AGCCGTGGTTGAATCTCTCATCTCTGTAGTACCGGATCGAATATGTGAGAGTCTCA 312
QY 182 AAGAAATCCCTTTAGAGTACCCAGCCAGGTCTGATCAACCGGATTAATACGAATTGA 241
Db AGGAAATGTCAATCAACGTGCTGAGCAGTGGCTGTACTCTGACATCAATGTAATCTGTC 372
QY 313 AGGAAATGTCAATCAACGTGCTGAGCAGTGGCTGTACTCTGACATCAATGTAATCTGTC 372
Db 242 CTGTGAGCGCATCATCTATTTTCAAGTAACCGATCCCAACTGCGCTCATACGGTTTGA 301
QY 373 AAATGATGAGTCTTTTACTGCGCATATGAGACCTTTACAGGCAAGCTACGGTGG 432
Db 302 GCAACTACATTATGCAATTAACCCAGCTTGGCCCAACGACGCTGGCTTATCGGGC 361
QY 433 AGGACCCGAGATATGCGGTCAACCCAGCTAGCTCAAAACCATGATCAAGAGCTCGGA 492
Db 362 GTATGAGTGTGACAAAACGTTTGAAGAAGCGGACGAATTAACAGTACGTCCTTCGG 421
QY 493 AACTCTCTGTGACAAAAGTCTTCCGGAAACGGAGGCTCTGAAGCCAGCATTTGTGATG 552
Db 422 CCTCGATGAAGCGCGCGGGCTTGGGGTGTGAAGTCTCTCGTTACGAATCAAGATT 481
QY 553 CCATCAACCAAGCTGTGATGCTGGGGTATCCGCTGCTGTTATGAGATCAAGATA 612
Db 482 TGGTTCCGCGCAAGAAATCTTTCGCGCAATGACGAGCAAAATTAACCGCGCAACGCAAA 541
QY 613 TCATATGTCACACCCGGGTGAAGAAGTCTATGAGATGACAGGTGAGAGGCGCGGA 672
QY 542 AACCGCGCCGTATTTGCGCAATTCGAAGGCGGTAAATCGAAACAATCAACTTGGCAATG 601
Db 673 AACCGGCCACAGTTCTTGAAGTCTGA-----GG 699
QY 602 GTACGCGTGAAGCGCAATTCGAATTCGAAGGCGAGGCTCAGGCTGCGGTCAATGCGT 661
Db 700 GGACCCGAGAGTCCGCTCATATGTGCAAGAGGAGAAACAGAGCCCAAGATCTTGGGCT 759
QY 662 CCATGCGCGAAGAAATGCGCGCATCAACGCGCCAAAGCGGAATCCCTGCGCC 721
```

Db 760 CCGAAGCGAAGAAAGCTGAACAGATTAATCAGACGACGAGAGAGGCCAATGATTTCTGG 819
Qy 722 TTGTTCCGGAAGCCAAATGCCGATCCGTAATTGCGCGCCCTTCAACCCAG 781
Db 820 CGAAGGCCAAGCTAAAGCTGAAGCTATTGAAATCCTGGCTGACGTCTGACAACTA 879
Qy 782 GCGGCGCGGATCGGTCAATCTGAAGATTGCGGAACATAGTAGCCGCTTCAACATC 841
Db 880 ATGAGATGCAACACTTCACTGACTGTGGCCGAGAGATGATGACGCGTTCTCCAAAC 939
Qy 842 TTGCGAAGAAAGCAATTCGCTATTATGCGCCCAATGTTGCCGACATCGGAGCTTA 901
Db 940 TGGCCAAAGACTCCCAACTATCTACTGCTTCCAACTTGGCGATGTCACAGCATG 999
Qy 902 TTTCTCGCGCATG 915
Db 1000 TGGCTCAGGCCATG 1013

RESULT 20
US-10-291-172-34
; Sequence 34, Application US/10291172
; Publication No. US20030228584A1
; GENERAL INFORMATION:
; APPLICANT: HySeq, Inc
; TITLE OF INVENTION: No. US20030228584A1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-045
; CURRENT APPLICATION NUMBER: US/10/291,172
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 09/693,267
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/665,363
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/616,847
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/596,193
; PRIOR FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 752
; SEQ ID NO 34
; LENGTH: 9098
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (75)..(9095)
US-10-291-172-34

Query Match 16.4%; Score 155.6; DB 17; Length 9098;
Best Local Similarity 50.6%; Pred. No. 4,4e-41;
Matches 432; Conservative 0; Mismatches 389; Indels 33; Gaps 1;

Qy 62 TCATCCCCCAGAGAGAGTCAAGTGTGCAAGAGGCTCGGCGCTTTTCATCGGCCCTGA 121
Db 193 TGTGTCCGACGACGAGAGGCTGTGGTGTGAGAGAAATGGGCCGATTCACCGGATCTGG 252
Qy 122 CGGCGCGTTGAATATTGTTGATTCCTTTATGCAACGCGCTGCGCTACCGGCATTGCTGA 181
Db 253 AGCTGTGTTGAACATCTCATCTCTGTGTGAGACCGGATCCGATATGTGCAAGTCTCA 312
Qy 182 AAGAAATCCCTTGAAGCTAACCCAGCAGGCTGCAATCAAGCGGAGTAATAGCAATTGA 241
Db 313 AGGAAATGTCTCAACAGTGTGAGAGAGTGGCTGTGACTTCTGACAAATGTAATCTGTG 372
Qy 242 CTGTGACGCGCATCATCTATTTCCTCAAGTAACCGATCCCAACTCGCTCATACGCTTCA 301
Db 373 AATGATGAGAGTCTTTACTGCTGACATATGAGACCTTAAAGGAAAGTACGAGTGG 432
Qy 302 GCAACTACATTAATGAGCAATTAACCCAGCTTGCACAAAGACGCTGCTTATGCGGC 361

Db 433 AGAAGCCGATGATATGCCGTCAACCCAGCTAGCTCAAAACAACATGATCAAGCTCGGCA 492
Qy 362 GTATGAGTTGAGACAAAAGCTTTGAAGAAGCGACGAAATCAAGATACCGTCTCTCG 421
Db 493 AACTCTCTCTGAGACAAAGTCTTCCGGAAACGGAGTCCCTGATGACGATTTGATG 552
Qy 422 CCGCTGATGAAGCCGCGGCGCTTGGGGGTGTAAGATCTCCGTTACGAAATCAAGATT 481
Db 553 CCATCAACCAAGCTGTCTACTGCTGGGTATTCGCTGCTCTCGTTATGATCAAGATA 612
Qy 482 TGGTTCCGCGCAAGAAATCTTCCGCAATGCAAGGCAAAATTACCCCGAACGCGAA 541
Db 613 TCCATGTCCACCCCGGTTGAAGATGTAATGCAAGTGAAGGAGGAGCGGCGGA 672
Qy 542 AACGCGCCGTATTTCCGAATCCGAAGCCGTAAATGAAACAATCAACTTGCATG 601
Db 673 AACGGGCCACAGTTCTAGATCTGA-----GG 699
Qy 602 GTACAGGTGAAGCCGAATTCGAATCCGAATCCGAAGGCGGCTCAGGCTGCGTCAATGCT 661
Db 700 GAGCCCGAAGTGGCCATCAATGTGCAAGAGGAAAGAACAGGCCCAAGATCTGGCT 759
Qy 662 CCAATGCCGAGAAATTCGCCGCAATCAACCGCGCAAGGCGAAGCGGAATCCCTGCGC 721
Db 760 CCGAAGCGAAGAAAGCTGAACAGATTAATCAGGACGAGAGAGGCGAGTCACTTCTG 819
Qy 722 TTGTTCCGGAAGCCAAATGCCGCAATCCGTAATTGCGCGCCCTTCAACCCAG 781
Db 820 CGAAGGCCAAGCTAAAGCTGAAGCTATTCGATCTGCTGCACTCTGACACAATA 879
Qy 782 GCGGCGCGATCGGTCAATCTGAAGATTGCGGAACATAGTAGCCGCTTCAACATC 841
Db 880 ATGAGATGCAACACTTCACTGACTGTGGCCGAGAGATGATGACGCGTTCTCCAAAC 939
Qy 842 TTGCGAAGAAAGCAATTCGCTATTATGCGCCCAATGTTGCCGACATCGGAGCTTA 901
Db 940 TGGCCAAAGACTCCCAACTATCTACTGCTTCCAACTTGGCGATGTCACAGCATG 999
Qy 902 TTTCTCGCGCATG 915
Db 1000 TGGCTCAGGCCATG 1013

RESULT 21
US-10-221-278-34
; Sequence 34, Application US/10221278
; Publication No. US20040034208A1
; GENERAL INFORMATION:
; APPLICANT: HySeq, Inc
; TITLE OF INVENTION: No. US20040034208A1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-045
; CURRENT APPLICATION NUMBER: US/10/221,278
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 09/693,267
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/665,363
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/616,847
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/596,193
; PRIOR FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 752
; SEQ ID NO 34
; LENGTH: 9098
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS

LOCATION: (75) .. (9095)
US-10-221-278-34

Query Match 16.4%; Score 155.6; DB 18; Length 9098;

Best Local Similarity 50.6%; Pred. No. 4.4e-41;
Matches 432; Conservative 0; Mismatches 389; Indels 33; Gaps 1;

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Oy 62 TCATCCCCCAGAGAAATCCAGTTCGAAAGGCTCGGCGTTTCCATCGCCCTGA 121
Db 193 TCGTCCCGCAGCAGAGGCTGGGTGTGAGCCGAATGGCCGATTCACCGGATCTCG 252
Oy 122 CGGCGGTTTGAATTTTGAATCCCTTTATCGACCGCGTGCCTACCGCATTCCTGA 181
Db 253 AGCGGTGTTGAATCCTCATCCCTGTGTTAGACCGGATCGGATATGTGAGAGTCTCA 312
Oy 182 AAGAAATCCCTTTAGACGTAACCCAGGCTGTGATCAGCGGCGATTAATGCAATGA 241
Db 313 AGGAAATGTGATCAACGTCGCTGAGAGTGGCTGTGATCTCGACATGTAACTCTGC 372
Oy 242 CTGTGACGGCATCATCTATTTCACAGTAACGATCCCAACTCGCTCATACGGTTTGA 301
Db 373 AATGATGAGAGTCTTTACCTGCGCATCATGSACTTTACAGGCAAGCTACGGTGTG 432
Oy 302 GCAACTACATTATGCAATTACCCAGCTTCCCAACGACGCTGCTTCCTTATCGGCG 361
Db 433 AGGACCTGAGTATCCGTCACCCAGCTAGCTCAAAACACATGATCAGAGCTCGCA 492
Oy 362 GTATGAGATTTGAGCAAAAGTTTGAAGAACGGACGAATCAACAGTACCGTCTCG 421
Db 493 AACTCTCTGTGACAAAGTCTTCGGGAAACGGAGTCCCTGAAATGCCAGATGGATG 552
Oy 422 CCTGCGATGAAGCCCGGCGCTTGGGGTGTGAAGTCTCCGTTACGAAATCAAGATT 481
Db 553 CCATTAACCAAGCTGTGATGCTGGGTATCCGCTGCTCGTTATGATGATCAAGATA 612
Oy 482 TGTGTCGCGCGAAGAAATCTTGGCGGATGCGGCAAAATTAACCGCGAAGCGGAA 541
Db 613 TCCATGTGTCACCCCGGGTGAAGAGTATGACAGATGACAGTGGAGGACAGCGCGA 672
Oy 542 AACCGGCGCGATTTGCCGAATCCGAAGGCCGTAATGAAACAATCAACCTTGCATG 601
Db 673 AACGGGCCACAGTCTTGAAGTCTGA-----GG 699
Oy 602 GTACGCGTGAAGCCGAAATCCAAACAATCCGAAGCGAGCTCAGCTCGGTCAATGCGT 661
Db 700 GGAACCCGAGAGTGGCCATCAATGTGGAGAAAGGAAACAGGCCCAAGTTCGCGCT 759
Oy 662 CCAATGCGGAGAAATGCGCCGATCAACCGCGCAAGCGAGCGGAATTCCTGCGCC 721
Db 760 CCGAAGCAGAAAGGCTGAACAGATAAATCAGGCGAGAGAGGCCAGTCAATTCG 819
Oy 722 TTGTTGGCGAAGCCAAATCCGAGCATCCGTAATTGCGCGCGCTTGAACCCGAG 781
Db 820 CGAAGGCGAAGGCTTAAGCTGAAGTATTCGAATCTGCTGCACTTGAACAACATA 879
Oy 782 GCGGGCGGAGATGCGGTCAATCTGAAGATTGCGGAAACAATAGTAGCCGCTTCAACATC 841
Db 880 ATGAGATGAGCAGAGCTTCACTGAGTGTGGCCGAGACATATGTCAAGCGGTTCCTCAAC 939
Oy 842 TTGCGAAGAAAGCAATAGCTGATTAATCCCGCAATGTTGCGGACATCGGAGCTGA 901
Db 940 TGGCGAAGAGCTCCAACTATCTCACTGCTCCAAACCTGGCGATGTCAACAGCATGG 999
Oy 902 TTTTCGCGCGCATG 915
Db 1000 TGGCTCAGGCGCATG 1013
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RESULT 22

US-09-898-216-2

Sequence 2, Application US/09898216

Patent No. US20020169308A1

GENERAL INFORMATION:

```
APPLICANT: Hillman, Jennifer L.
Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,216
FILING DATE: 02-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/781,562
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0181 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1188 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Consensus
CLONE: Consensus
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-898-216-2
Query Match 16.4%; Score 155.2; DB 9; Length 1188;
Best Local Similarity 50.5%; Pred. No. 2.1e-41;
Matches 431; Conservative 0; Mismatches 390; Indels 33; Gaps 1;
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Oy 62 TCATCCCCCAGAGAAATCCAGTTCGAAAGGCTCGGCGTTTCCATCGCCCTGA 121
Db 182 TCGTCCCGCAGCAGAGGCTGGGTGTGAGCCGAATGGCCGATTCACCGGATCTCG 241
Oy 122 CGGCGGTTTGAATTTTGAATCCCTTTATCGACCGCGTGCCTACCGCATTCCTGA 181
Db 242 AGCGGTGTTGAATCCTCATCCCTGTGTTAGACCGGATCGGATATGTGAGAGTCTCA 301
Oy 182 AAGAAATCCCTTTAGACGTAACCCAGGCTGTGATCAGCGCGGATTAATGCAATGA 241
Db 302 AGGAAATTTGATCAAGTGTGCTGAGCAGTGGCTGTGATCTCGAACAATGATCTGCG 361
Oy 242 CTGTGACGGCATCATCTATTTCACAGTAACGATCCCAACTCGCTCATACGGTTTGA 301
Db 362 AATGATGAGAGTCTTTAATCTGCGCATCAATGACCTTCAAGGCAAGCTACGGTGTG 421
Oy 302 GCAACTACATTATGCAATTACCCAGCTTGGCCAAACGACGCTGCTTCGTTATCGGCG 361
Db 422 AGGACCTGAGTATCCGTCACCCAGCTAGCTCAAAACAACATGATCAGAGTCTCGCA 481
Oy 362 GTATGAGATTGACAAAAGTTTGAAGAACGCGACGAATCAACAGTACGTCGTCGCG 421
Db 482 AACTCTGTTGAGCAAAAGTCTTCGGGAAAGGAGTCCCTGGAATGCAAGATTTGATG 541
Oy 422 CCTCGATGAAGCCCGGCGGCTTGGGGTGTGAAGTCTTCGTTACGAATCAAGATT 481
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OY	120	GACGGCCGGTTGGAATATTTTGATTGATTCCTTTATGCACCGCGTGCCTACCGCATTTGGCT	179
Db	370	CGGCTCCGGGTTCCACCTCTCTATGCCCGCGCGACCGGATTTGGCTTACGTGACTCGCT	429
OY	180	GAAGAATAATCCCTTTAGAGGTACCCGACGAGGTCTGCATACGCGGATATATGCAATT	239
Db	430	CAAGAGAAGACCATTCCTTATCCCTACCAAGAAAGCGCATTCACCAAGAGCAACGTCAACAT	489
OY	240	GACTGTGACGGCATCATCTATTTCCAAAGTAACCGATCCCAAACTGCGCTCATACGGTTT	299
Db	490	ACAGATTGCACGCGTCATCTATGTCAAGATCATGAGACCCCTACCTTGCTTCTCATATGGTGT	549
OY	300	GAGCAACTCATATTATGCGCAATTAACCGAGTGGCCAAAGAGCGTGCCTTCGGTTATTCG	359
Db	550	GGAGATCCCAATCTATGTCTGTCTCTACACTTGCACAAACAAACCATGAGAAATGAACTCG	609
OY	360	GCGTATGAGATTGGAACAATAAGTTTGAMAGACGCGACGAATTCAGACTACGTCGTCTC	419
Db	610	GAAGATTAACCTTATAGATTAAGACTTTTGAAGAGAGATGCACTTAAATGAGAAATTTGTGAG	669
OY	420	CGCCCTCGATGAAGCGCGCGGGCTTGGGGTGTGAATGTCCTCCGTTACGAATTCAAAGA	479
Db	670	TGCCCATCATGAAAGCAGCCACAGATTGGGGCCCTGAAGTGTATCCGCTATAGGATCAGGA	729
OY	480	TTTGGTTCGGCGCAAGAATCCTTGCGCCAAATGACAGCAAAATTAACGCCCAAGCGCA	539
Db	730	CATAAATCCTCCAGCAGGAGATTAGGAGGCTATGAGAGATGCAAGCTGAGGCAAAAGGAA	789
OY	540	AAAACGCGCGCGTATTTGCCGAATCCGAGGCGCGTAATAATGCACAAATC	588
Db	790	AAAAAGCGGCTCAATCTTGAAGTCAGAAAGGAAATGAAACAGGCCCAATTC	838

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RESULT 25
US-10-425-115-13230
/ Sequence 13230, Application US/10425115
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
/ TITLE OF INVENTION: Plants
/ FILE REFERENCE: 38-21(53222)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 369326
/ SEQ ID NO 13230
/ LENGTH: 805
/ TYPE: DNA
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: MRT4577_112059C.1
US-10-425-115-13230

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Query Match	15.0%;	Score 142.2;	DB 20;	Length 805;
Best Local Similarity	53.5%;	Pred. No. 4.6e-37;		
Matches 297;	Conservative	0;	Mismatches 258;	Indels 0;
				Gaps 0;

QY	60	CGTCATCCCCCAGCAGAAAGTCACGTTGTGCCAAAGAGCTCGGGCGTTTCCATCGCGCCT	11.9
Db	216	CATCGTCGCGGAGAAAGAGCCCTTCGTGATGAGCCCTTCGGCAAGTACCTCAAGAGCT	27.5
QY	120	GACGCGCCGTTTGAATATTTTGATTCCCTTATACACCGCGTGCCTACCGCCATTGCT	17.9
Db	276	CGACTCCGGGATCCAGGCGCTCGTCCCTCGTCGACCGGATGCGCTACGTGACCTCTCT	33.5
QY	180	GAAAGAAATCCCTTTAGAGTACCCAGCAGGCTCTGCATCAGCGCGGATTAATAGCAATT	23.9
Db	336	CAAGGAGGAAGCATTCCTCCATCCCGACCAAGTCGCTATCACCAAGAGTAACTGTGCAT	39.5

QY	240	GACTGTGACGGC	ATCATCTATTTC	CCAGTAACGAT	ATCCCAATCG	CGCTCATAGG	TTG	239	
Db	336	CCAGATGACCGC	CGCTCTCTACG	TCAAGATGTGAT	CTCTACCGCTT	CCATATGG	CGT	455	
QY	300	GAGCAACTACAT	TATATGGCAATTA	CCAGCTTGCC	CAAAAGACGCTG	CTTCGTTATCG	359		
Db	436	GAGGATCCCAT	TTTTTGTGATCT	CACTTCGCGAC	AGCAATATGAA	AGTAGAGCTT	GG	515	
QY	350	GCGTATGAGATT	GACAAACGTTT	GAAGAACGCG	ACGAAATCA	CAGTACGTCG	CTC	419	
Db	516	AAAGATAACCT	TGGACAGAACT	TTTGAAGAGAG	AGACACATTGAAT	GAGAAAGTTGTG	AG	575	
QY	420	CGCCCTCGAT	GAAAGCCCGG	GGGCTTGGG	GTGAAAGTCTCC	GTTACGAATCA	AGAA	479	
Db	576	GTCCATAATG	AGGCTTGC	ACAGACTGGGG	CTTGAAGTCTCT	CGTTATGAGATC	AGGA	635	
QY	480	TTTGGTTCCG	CGCAAGAAAT	CTTCGGCG	CATGACGCAAA	TTACCGCGCA	CGCGA	539	
Db	636	CATTTCTCT	CCACCGGGG	GTGAAGATG	CTATGGAGATC	AGACAGAGG	CAAGAAAGAG	695	
QY	540	AAAAAGCGCC	CGTATTTGCG	ATCCGAAGCC	GTAAATCGA	CAAAATCAAT	CAATCACTT	CCAG	599
Db	636	AAAGGTGT	CAAAATTTCT	CAAGTCAAG	AGGGGCTAT	GTGGATCAG	CAAAACGG	CGCAAA	755
QY	600	TGCTCAGCGT	GAAGC	614					
Db	756	AGGTAGGCTG	GAAGC	770					

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RESULT 26
US-10-425-114-21145
/ Sequence 21145, Application US/10425114
/ Publication No. US2004003488A1
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Jingdong
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Screen, Steven E
/ APPLICANT: Tabaska, Jack E
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21531313B
/ CURRENT APPLICATION NUMBER: US/10/425, 114
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 73128
/ SEQ ID NO 21145
/ LENGTH: 1123
/ TYPE: DNA
/ ORGANISM: Zea mays
/ FEATURES:
/ OTHER INFORMATION: Clone ID: LIB3279-059-F3_FLI
US-10-425-114-21145

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Query Match	14.0%;	Score 133;	DB 18;	Length 1123;
Best Local Similarity	52.7%;	Pred. No. 7.3e-34;		
Matches 338;	Conservative 0;	Mismatches 270;	Indels 33;	Gaps 1;

QY	245	TTGACGGCATCATCTATTATTTCCAGTAACCGATCCCAAACGTGGCTCATACGGTTGAGACA	304
Db	7	TTGACAGCGTCATCTATGTCTCAAGATCAACGAGACCCCTACCTTGCTTCCTATAGGTGAGAGA	66
QY	305	ACTACATTAATGSGCAATTAACGAGCTGGCCAAACGAGCGTCGGTTCCGTTATCGGGACGTA	364
Db	67	ATCCATCTTAATGCTGTCTCTACACTCTTGACAAACACCATGAGAGTAACTCGGGAAGA	126
QY	365	TGAGATTGACAAAACGTTTGAAGNACCGACGAAATCAACAGTACCGTCTTCGCGCC	424
Db	127	TAACTTGATTAAGACTTTTGGAGGAGAGATGCAATTAATGAGAAAATTGTAAGTGCACA	186
QY	425	TCGATGAAGCCGCGGGGCTGGGGGTGGAAGTCTCCGTTACGAATCAAGAGATTGGG	484
Db	187	TCATATGAAGCACCAAGATTGGGGCTCGAAGTGTATCCGCTATGATCGGGGACATPA	246

QY 485 TTCGCCGCGAGAAATCTCTGCGCGATGCAAGGCAAAATTAACCCGCCGAGCGGAAAAAC 544
DB 247 ATCTCCGAGCAGAGGATTAGGCGAGGCTATGAGATGACAGGCTGAGGCAAGAAAGAAAAAC 306
QY 545 GCGGCCGATGATGCGGATCCGAAAGGCGGTAATAATGAAACAATCAACCTTGCAGTGGTC 604
DB 307 GGGCTCAATCTTGTAGTCAAGAGGAGTAAA----- 338
QY 605 AGCGTGAAGCCGAAATCCAAACAATCCGAGGAGCTCAGGCTGCGGTCAAATGCGTCA 664
DB 339 -----CAGGCCCAATTCCTTGATCAGAAAGGAAAAAGATCCCAAGATCTTGTATCTG 393
QY 665 ATGCGGAGAAATCGCCCGCATCAACCGCGCCAAAGGCGAAGCGGAATCTTCCGCTTG 724
DB 394 AAGGAGCTATGTGTATGATCAGCAACCGTGCAGAGGCTGCGCTGAAAGCAATTCCTTGCA 453
QY 725 TTGCGGAGCCCAATGCCAAGCCATCCGTCAAATGCGCGCGCTTCAAAACCAAGGCG 784
DB 454 AGTCAGAAAGCTACTCTGCTGGAATGAGATTGGTTCAAGATGACATGACATGAAAGCA 513
QY 785 GGGCGGATGCGGTCAATCTGAAGATTGCGGAAACAATACCTAGCCGCTTCAACAATCTTG 844
DB 514 GTGCGCAAGGCTGCTAGCTGGAACCTTGAGAGCAATACATGAGGATTTCAAAATCTGG 573
QY 845 CCAAGAAAGCAATACGCTGATTAATGCGCGCCCAATGTTGCC 885
DB 574 CACAAAGCAATACATGCTTCTTCCAGGTGATAGTCC 614

RESULT 27

US-10-437-963-76661
; Sequence 76661, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Bouharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 76661
; LENGTH: 727
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_76636C.1
US-10-437-963-76661

Query Match 13.4%; Score 126.8; DB 19; Length 727;
Best Local Similarity 55.8%; Pred. No. 7.6e-32;
Matches 242; Conservative 0; Mismatches 192; Indels 0; Gaps 0;
QY 60 CGTCATCCCGCAGCAGAGTCACGTTGTCAAGAGCTCGGCGCTTCCTCAATCGCGCT 119
DB 246 CATGCGCGGAGAAAGAGCGCTTCGTGTGAGCGGTTTCGCAAGTACGTCAAGAGCGCT 305
QY 120 GACGCGCGGTTGAATATTGATTCCCTTAATCGACCGCGTGCCTTACCGCATTCGCT 179
DB 306 CGGCTCGGAGATCCACGTCTGCTCCCTCGTGAACGCGATCGCTACGTCACTCGCT 365
QY 180 GAAAGAAATCCCTTGAAGTACGTAACGACGAGTCTCATCAGCGGATTAATACGANT 239
DB 366 CAGGAGAGGAGCATCCCATCCCGACAGTCCGCAATCAAGAGCAACGCTTCAT 425

QY 240 GACTGTGACCGCATCATCTATTTCAGTAACGATCCAAACTCGCTCATACGTTTC 299
DB 426 CCAATGACACGCGCTCTTAAGTACATGTTGATCTCCATACCTTGGCTTATGATG 485
QY 300 GAGCACTACATTAATGCAATTAACCACTTGGCCCAACGACGCTCGTTCCGTTATGG 359
DB 486 GGAGAAATCAATTTTTCAGTCAATACAGCTTGGCCCAACCACTATGAGAGTACGCTGG 545
QY 360 GCGTATGAGATTGCAAAACGTTTGAAGACGAGCAATCAACAGTACCGTCTTC 419
DB 546 AAGATTAAGCTAGCAAGACTTTTGAAGAGAGATACATAATGAGCAATTTGAG 605
QY 420 CGCCCTGATGAAAGCGCGGCGCTTGGGGTGTGAAGTCTTCCGTTAGAAATAGGA 479
DB 606 GTCCATTAATAGGCTGCAACTGATTTGGGAGCTGAAATGCTTCCGTTATGAGATCAGGA 665
QY 480 TTTGGTCCGCGC 493
DB 666 TATATCTCCGCGAC 679

RESULT 28

US-09-878-134-349
; Sequence 349, Application US/09878134
; Publication No. US20020086303A1
; GENERAL INFORMATION:
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: King, Gordon B.
; APPLICANT: Xu, Jianshun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 21021.532
; CURRENT APPLICATION NUMBER: US/09/878,134
; CURRENT FILING DATE: 2001-06-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 349
; LENGTH: 732
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-878-134-349

Query Match 13.4%; Score 126.8; DB 9; Length 732;
Best Local Similarity 49.7%; Pred. No. 7.6e-32;
Matches 323; Conservative 0; Mismatches 327; Indels 0; Gaps 0;
QY 85 GTTGCGAAAGGCTCGGGGCTTTCATCGCGGCTGACGCGGCTTGAATATTGATT 144
DB 6 GTGTGAGCGAATGAGCGCGATTCACCGGATCTCGAGCTGTGTAACATCTCATC 65
QY 145 CCTTATCGACCGCGCTGCTACCGCAATTCGTAAGAAATCTTTAGACGTACC 204
DB 66 CCGTGTATGACCGGATCGGATATGAGAGTCTCAAGAAATGTCAACGCGCT 125
QY 205 ACCGAGGTGATCAACGCGGATTAATAGCAATGACTGTGAGCGCATCATATTTC 264
DB 126 GAGCAGTGGCTGTGATCTTCGACAAATGTAACCTGCAATGAGAGTCTTTACCTG 185
QY 265 CAAGTAACGATCCCAACTCGCTCATCGGTTGAGAGCACTAATTAATGCAATTACC 324
DB 186 CCGATCATGAGACCTTTCAAGGCAAGCTACGAGTGTGAGAGACCTGAGATGCCGTCAC 245
QY 325 CAGCTTGCCCAAGCAGCGCTGCTTCGTTATCGGCGGTATGAGTGAAGCAAAAGCTTT 384
DB 246 CAGCTTAGCTCAAAACAACATGAGATCAGAGCTCGGCAAACTCTCTGGAACAAAGCTTC 305
QY 385 GAAAGACGAGCAAAATCAACAGTACCGTCTCCGCTCGAGTGAAGCGCGCGGCT 444
DB 306 CGGAAACGGAATCCCTGAATCCAGCATTTGAGATGCCATACCAAGCTCTGACTGC 365
QY 445 TGGGGTGAAGTCTCTCGCTACGAAATCAAGATTTGGTTCCGCGCAAAATCTCT 504

Dh 366 TGGGATATCCGTCGCTCCGTTATGATGATCAAGATATCCATGTGCAACCCCGGGTGA 425
Qy 505 CGCCCAATGACGACCAATTAACCGCCGAGCCAAAACCGCCCGATATGCCGAATCC 564
Db 426 GAGTCTATGACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGT 485
Qy 565 GAAAGCCGCTAAATGCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 624
Db 486 GAGGGAGCCGAGAGTGGCCATCAATGTGCAAGAGGAGGAGGAGGAGGAGGAGGAG 545
Qy 625 CAATCCGAGGAGGAGTCAAGTCCGCTCAATGCTCAATGCTCAATGCTCAATGCT 684
Db 546 GCTTCGGAAGCAAGAAAGCTGAACAGTAATCAAGAGAGAGAGAGAGAGAGAGAG 605
Qy 685 ATCAACCGCGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 734
Db 606 CTGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 655

RESULT 29

US-10-767-701-5816
; Sequence 5816, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5353)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 5816
; LENGTH: 742
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(742)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MA03-CLUS25744_1
US-10-767-701-5816

Query Match 13.2%; Score 124.8; DB 19; Length 742;
Best Local Similarity 55.1%; Pred. No. 3.7e-31;
Matches 243; Conservative 0; Mismatches 198; Indels 0; Gaps 0;

Qy 60 CGTATCCCGCAGGAGATCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 119
Db 297 CATAGTCCCGAGAGAGAGGCTTGTGTATGAGAGGTTCCGGAAGTATCTCAAGAGCT 356
Qy 120 GACGCGCGGTTGATATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 179
Db 357 CGGCTCGGGTTTCAAGTCTGATCCCGCGTGAACGTAATGCTAAGTCAAGTCAAG 416
Qy 180 GAAAGAAATCCCTTAGACGTAACGAGGAGTGTGATCAAGGCGGTAATAGCAATT 239
Db 417 CAAGAGAGAGCAATCCCATCCCGCACAGAACCCATCAACAGAGAGAGAGAGAGAG 476
Qy 240 GACTGTGAGCGGATCATCTATTTTCAAGTAAAGGATCCCAACTCGCTCATAGCGTTC 299
Db 477 ACAGATGACAGCGTCAATCTATGTAAGATCAAGAGCCCTAATCTTCTCTATGTGT 536
Qy 300 GAGCAACTACATTAATGCAATTAACCACTGCGCCAAACGAGCGTCCGCTTATGCG 359
Db 537 GGAAGATCAATCTATGCTGTCTCACTCACTGCAAAACAGAGAGAGAGAGAGAGAG 596
Qy 360 GCGTATGAGTGTGCAAAAGCTTTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 419
Db 597 GAAGTAACTTTAGCAAGAGCTTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 656

Qy 420 CGCCCTGATGAACCGCCGAGGCTTGAGAGTGTGAAGTCTCCGTTACGAATCAAGGA 479
Db 657 TGCCATCAATGAGACAGCACAGATTTGGGGCTGAAGTATATCGGTATGAGATCAGGA 716
Qy 480 TTTGTTCCGCGCCAGAGAAAT 500
Db 717 CATTAATCTTCCNAATGAGAT 737

RESULT 30

US-10-425-114-19667
; Sequence 19667, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 19667
; LENGTH: 1091
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3150-091-G4_FLI
US-10-425-114-19667

Query Match 12.3%; Score 117; DB 18; Length 1091;
Best Local Similarity 51.9%; Pred. No. 2e-28;
Matches 316; Conservative 0; Mismatches 260; Indels 33; Gaps 1;

Qy 277 CCCAACTCGCCCTCATGAGGTTGAGCAATCAATTAATGCAATTAATCAATCAATCAAT 336
Db 2 CCTTACTTCTTCTTATGTTGTTGAGATCAATCTATGCTGTCCATCAATCTTGCACAA 61
Qy 337 ACGAGCTGCGTTCCTTATCGGCGTATGAGATTTGAACAAACGTTTGAAGAACGAG 396
Db 62 ACAACATGAGAGATGAAGTGGAGAGATTAACCTTAATGAAGTCTTGAAGAGAGAT 121
Qy 397 GAAATCAAGATACCTGCTGCTCCGCTCGATTAACCGCGGCGCTTGCGGTGATAA 456
Db 122 GCATTAATGAGAAATTTGATGTCATCAATGAAGAGAGAGAGAGAGAGAGAGAG 181
Qy 457 GTCTCGGTTGCAATCAAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 516
Db 182 TGTATCGCTATGAGATCAAGGACATTAATCTCTACAGAGGATTAAGCAGGCTATGAG 241
Qy 517 GCACAAATTAACCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 576
Db 242 ATGAGGCTGAG 301
Qy 577 ATGCAAAATCAACTTTCAGTGTCAAGGAGGAGAGAGAGAGAGAGAGAGAGAGAG 636
Db 302 -----CAGGCCCAAAATCTTGAATCAAGAGG 328
Qy 637 GAGGCTCAGGCTGCGTCAATGCTCCAAATGCGAGAAATCGCGCGATCAACCGCGCC 696
Db 329 AAAAAAGTGCAGATCTTGAATCTGAAGAGACTATGTTGATCTTAGCAAAACCTGTC 388
Qy 697 AAGGCGAAGGAGATCTGCGCTTGTGTCGAGAGCAATGCGAGAGAGAGAGAGAGAG 756
Db 389 AAGGCTGCGTGAAGATCTTTCGCAAGTCAAGAGTACTGCTCGGGAATGAGATTG 448
Qy 757 ATTGCGCGCGCTTCAACCCAGAGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 816
Db 449 GTTTCAGATGAG 508

Qy 817 CAAATGACCCCGCTTCAACATTTGGCAAGAAAGCATACGCTGATTTAGCCGCC 876
Db 509 CAAATGACGAAAGCATCTTCAATCTGGCAAAAGACAAATATACATGCTTCTCCAGGT 568
Qy 877 AATGTTGCC 885
Db 569 GATAGTGCC 577

RESULT 31

US-09-922-217-1031
; Sequence 1031, Application US/09922217
; Patent No. US2002076414A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tonglong
; APPLICANT: Jiang, Yudi
; APPLICANT: Smith, Carole Lynn
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.471C13
; CURRENT APPLICATION NUMBER: US/09/922,217
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1031
; LENGTH: 518
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 443
; OTHER INFORMATION: n = A,T,C or G
US-09-922-217-1031

Query Match 11.7%; Score 111.2; DB 9; Length 518;
Best Local Similarity 51.8%; Pred. No. 1.3e-26;
Matches 251; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

Qy 85 GTTTCGAAAGGCTCGGGGCTTTCATCGCGCCCTGACGCGCGGTTGAAATTTTGATT 144
Db 6 GTGTGGAGCGAATGGCCGATTCACCGAGTCTTGAGCTGTGAAATCTTCATC 65
Qy 145 CCCTTATGACCGCGCTGCTACCGCATTTGCTGAAAGAAATCCCTTTAGACGTACC 204
Db 66 CTGTGTATGACCGAGTCGATATGTGCAAGAGTCTTAAGAAATTTGTCTCAACGTGCT 125
Qy 205 AGCCAGTCTGCATCAACGCGCATTAATGCAATTTGACTGTGACCGCATCTAATTC 264
Db 126 GAGCAGTCTGCTGTGATCTTCGACATGTAATCTGCAATGATGAGAGTCTTTAAG 185
Qy 265 CAAGTAACCGATCCAACTCGCTTATACGTTGACGAACTAATTTATGCAATTAAC 324
Db 186 CCATCATGAGACCTTAACAGGCAAGCTACGCTGTGAGAGACCTGATGATGCGTCAAC 245
Qy 325 GAGCTTGCCCAACGACGCTGCTGCTTATGCGCGATGAGATTTGACAAAGCTTT 384
Db 246 GAGCTAGCTCAACCAACATGATGATGAGCTGCGAAATCTCTCTGACAAAGCTTTC 305
Qy 385 GAAGAACGCGACCAAAATCAACAGTACCTGCTCGCGCTCGATGAAAGCGCGGAGCT 444
Db 306 CGGGAACGGAGGCTCGTGAATGCAAGATTTGTGAGATGATCAACAGCTGCTGAC 365
Qy 445 TGGGATGTGAAGTCTCTCGTTACGAATATCAAGATTTGTTCCGCGCAAGAAATCTTT 504

Db 366 TGGGATATCCCGCTGCTCTGTTATGATCAAGATATCAATGTCACCCCGGTGAA 425
Qy 505 CGCGCATGACGAGCAAAATTAACGCGCGAAGCGGAAAGCGCGCTATTTGCCAATCC 564
Db 426 GAGTCTATGACAGATGATGAGAGGAGAGGCGGAAACGCGCACAGTTCTAGAGTCT 485
Qy 565 GAAGG 569
Db 486 GAGGG 490

RESULT 32

US-09-833-263-1031
; Sequence 1031, Application US/09833263
; Patent No. US20020110547A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Stolk, John A.
; APPLICANT: Meagher, Madeleine J.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; FILE REFERENCE: 210121.471C12
; CURRENT APPLICATION NUMBER: US/09/833,263
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1031
; LENGTH: 518
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(518)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-263-1031

Query Match 11.7%; Score 111.2; DB 9; Length 518;
Best Local Similarity 51.8%; Pred. No. 1.3e-26;
Matches 251; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

Qy 85 GTTTCGAAAGGCTCGGGGCTTTCATCGCGCCCTGACGCGCGGTTGAAATTTTGATT 144
Db 6 GTGTGGAGCGAATGGCCGATTCACCGAGTCTTGAGCTGTGAAATCTTCATC 65
Qy 145 CCCTTATGACCGCGCTGCTACCGCATTTGCTGAAAGAAATCCCTTTAGACGTACC 204
Db 66 CTGTGTATGACCGAGTCGATATGTGCAAGAGTCTTAAGAAATTTGTCTCAACGTGCT 125
Qy 205 AGCCAGTCTGCATCAACGCGCATTAATGCAATTTGACTGTGACCGCATCTAATTC 264
Db 126 GAGCAGTCTGCTGTGATCTTCGACATGTAATCTGCAATGATGAGAGTCTTTAAG 185
Qy 265 CAAGTAACCGATCCAACTCGCTTATACGTTGAGCAATTAATTTATGCAATTAAC 324
Db 186 CCATCATGAGACCTTAACAGGCAAGCTACGCTGTGAGAGACCTGATGATGCGTCAAC 245
Qy 325 GAGCTTGCCCAACGACGCTGCTTATGCGCGATGAGATTTGACAAAGCTTT 384
Db 246 GAGCTAGCTCAACCAACATGATGATGAGCTGCGAAATCTCTCTGACAAAGCTTTC 305
Qy 385 GAAGAACGCGACCAAAATCAACAGTACCTGCTCGCGCTCGATGAAAGCGCGGAGCT 444
Db 306 CGGGAACGGAGGCTCGTGAATGCAAGATTTGATGATGATGATGATGATGATGATGAT 365
Qy 445 TGGGATGTGAAGTCTCTCGTTACGAATATCAAGATTTGTTCCGCGCAAGAAATCTTT 504
Db 366 TGGGATGTGCTGCTCTCTGTTATGATGATGATGATGATGATGATGATGATGATGAT 425
Qy 505 CGCGCATGACGAGCAAAATTAACGCGCGAAGCGGAAAGCGCGCTATTTGCCAATCC 564
Db 426 GAGTCTATGACAGATGATGAGAGGAGAGGCGGAAACGCGCACAGTTCTAGAGTCT 485

OY 565 GAAG 569
DB 486 GAGG 490

RESULT 33

US-10-025-380-1031
Sequence 1031, Application US/10025380
Publication No. US20020182191A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Stolk, John A.
APPLICANT: Wang, Tongtong
APPLICANT: Jiang, Yugu
APPLICANT: Smith, Carole L.
APPLICANT: King, Gordon E.
APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick Thomas S.
APPLICANT: Carter, Darick
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C14
CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 1129
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1031
LENGTH: 518
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 443
OTHER INFORMATION: n = A,T,C or G
US-10-025-380-1031

Query Match 11.7%; Score 111.2; DB 13; Length 518;
Best Local Similarity 51.8%; Pred. No. 1.3e-26;
Matches 251; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

OY 85 GTTGTGAAAGGCTCGGGCGTTTCCATCGCGCCCTGACGGCGGTTTGAATATTTGATT 144
DB 6 GTGGTGAAGCGAATGGCGGATTCACCGGATCTCGAGCGCTGGTTGAACTCTCATC 65
OY 145 CCTTTATCGACCGCGTGGCTTACCGCATTCGCTGAAAGAAATCCCTTTAGACGTACC 204
DB 66 CCGTGTGTAAGACCGGATCGATATGTGCAAGTCTCAAGAAATGTGATCAACGTGCT 125
OY 205 AGCCAGGTCTGATCAGCGCGGATTAATGCAATGACTGTGAGCGCATCATCTATTC 264
DB 126 GAGCAGTGGCTGTACTCTGACAAATGTAATCTGCAATGATGAGTCTTTTACTG 185
OY 265 CAAGTAACCGATCCCAACTGCGCTCATACGTTTGCAGCAACTATTAATGCAATTACC 324
DB 186 CGCATATGAGACCTTACAGGCAAGCTACGCTGTGAGAGACCGGATATGCGGTACC 245
OY 325 CAGCTTGGCCAAAGAGCGTGGTTCGTTATCGGGCGTATGAGTTGACAAACGTTT 384
DB 246 CAGCTAGCTCAAAACCAACCATGATCAGAGCTCGCAAACTCTCTGCAAAAGTCTTC 305
OY 385 GAAGAACCGCAAGAAATCAACAGTACGTCGCTCCCGCTCGATGAGAGCGCGCGGCT 444
DB 306 CGGAAACGGAGTCCCTTAATGCGAGCATGTGATGATCAACAAAGTGTGACTGC 365
OY 445 TGGGTTGAAAGTCTCCGTTACGAATCAAGATTTGTTCCGCCCAAGAAATCCTT 504

DB 366 TGGGTTATCCGCTCTCCGTTATGATCAAGGATATCATGTCACCCCGGGTAAA 425
OY 505 CGCCATGCAAGCAAAATTAACCGCCGAACGCAAAAACCGCCGATATGCGGATCC 564
DB 426 GAGTCTATGAGATGAGATGAGAGGAGAGCGGGAACCGGCCACAGTTCTAGACT 485
OY 565 GAAG 569
DB 486 GAGG 490

RESULT 34

US-09-998-598-841
Sequence 841, Application US/0998598
Patent No. US20020150922A1

GENERAL INFORMATION:

APPLICANT: Stolk, John A.
APPLICANT: Xu, Jiangchun
APPLICANT: Chenault, Ruth A.
APPLICANT: Meagher, Madelein Joy
TITLE OF INVENTION: DIAGNOSIS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.561
CURRENT FILING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 2606
SOFTWARE: Corlika Invention Disclosure Database
SEQ ID NO 841
LENGTH: 504
TYPE: DNA
ORGANISM: Homo sapiens
US-09-998-598-841

Query Match 11.7%; Score 110.6; DB 9; Length 504;
Best Local Similarity 51.8%; Pred. No. 2e-26;
Matches 251; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

OY 85 GTTGTGAAAGGCTCGGGCGTTTCCATCGCGCCCTGACGGCGGTTTGAATATTTGATT 144
DB 6 GTGGTGAAGCGAATGGCGGATTCACCGGATCTCGAGCGCTGGTTGAACTCTCATC 65
OY 145 CCTTTATCGACCGCGTGGCTTACCGCATTCGCTGAAAGAAATCCCTTTAGACGTACC 204
DB 66 CCGTGTGTAAGACCGGATCGATATGTGCAAGTCTCAAGAAATGTGATCAACGTGCT 125
OY 205 AGCCAGGTCTGATCAGCGCGGATTAATGCAATGACTGTGAGCGCATCATCTATTC 264
DB 126 GAGCAGTGGCTGTACTCTGACAAATGTAATCTGCAAAATGATGAGTCTTTTACTG 185
OY 265 CAAGTAACCGATCCCAACTGCGCTCATACGTTTGCAGCAACTATTAATGCAATTACC 324
DB 186 CGCATATGAGACCTTACAGGCAAGCTACGCTGTGAGAGACCGGATATGCGGTACC 245
OY 325 CAGCTTGGCCAAAGAGCGTGGTTCGTTATCGGGCGTATGAGTTGACAAACGTTT 384
DB 246 CAGCTAGCTCAAAACCAACCATGATCAGAGCTCGCAAACTCTCTGCAAAAGTCTTC 305
OY 385 GAAGAACCGCAAGAAATCAACAGTACGTCGCTCCCGCTCGATGAGAGCGCGGCT 444
DB 306 CGGAAACGGAGTCCCTGAATGCGAGATGTGATGATCAACCAAGCTGTGACTGC 365
OY 445 TGGGTTGAAAGTCTCCGTTACGAATCAAGATTTGTTCCGCCCAAGAAATCCTT 504
DB 366 TGGGTTATCCGCTCTCCGTTATGAGATCAAGATTCATGTGCAACCCCGGTTAAA 425
OY 505 CGCCATGCAAGCAAAATTAACCGCCGAACGCAAAAACCGCCGATATGCGGATCC 564
DB 426 GAGTCTATGAGATGAGATGAGAGGAGAGCGGGAACCGGCCACAGTTCTAGACT 485
OY 565 GAAG 569
DB 486 GAGG 490

```
RESULT 35
US-09-998-598-58
; Sequence 58, Application US/09998598
; Patent No. US20020150922A1
; GENERAL INFORMATION:
; APPLICANT: Stolk, John A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Megawer, Madelein Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.561
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 2606
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 58
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-998-598-58

Query Match      11.6%; Score 110.4; DB 9; Length 563;
Best Local Similarity 53.5%; Pred. No. 2.5e-26;
Matches 211; Conservative 0; Mismatches 201; Indels 0; Gaps 0;

QY      62 TCATCCCCGAGGAGGATCCAGCTTGTGAAAGGCTCGGGCGTTCCATCGGCCCTGA 121
DB      124 TGTGTCGCGAGCGAGGCGCTGGGTGTGAGGAAATGGGCCGATTCCACCGGATCTGG 183
QY      122 CGCGCGGTTGAATATTTTGAATTCCTTTATCGACCGCGTCCGCTAACCGCATTCGCTGA 181
DB      184 AGCTGTGTTGAACATCTTCATCCCTGTGTGAGACCGGATTCGATATGTGAGAGTCTCA 243
QY      182 AAGAAATCCCTTTAGACGTACCCAGCAGGTCTGCATCAAGCGCGGTAATAGCAATTTGA 241
DB      244 AGGAAATGTCAATCAACGTGCGCTGAGCAATCGGCTGTGACTTCGCAATGTAACTCTGC 303
QY      242 CTTGTGAGGCGCATCATCTATTTCCAGTAACGATCCCAACTCGGCTCATACGTTTGA 301
DB      304 AATTCATGAGATCTTTTACCTGCGCATATGACCTTTCAAGGACAGATACGATGTGG 363
QY      302 GCAACTACATTTATGCAATTAACCCAGCTTGCCTCCCAAGCAGCGTCCGTTATCGAGC 361
DB      364 AGGACCTGAGTATGCGCTCAACCCAGCTAGCTCAAAACACATGATACAGAGCTGGCA 423
QY      362 GTATGAGTTGACAAACGTTGAAAGACGAGCAAAATCAACAGTACCGTGTCTCG 421
DB      424 AACTCTCTCGGACAAAGTCTTCGAGGAAAGGAGTCCCTGAATGCGAGCATTTGTGATG 483
QY      422 CCTCATGAGAGCGCGCGGGGCTTTGGGGGTGAAATCCCTCCGTTACGAATCAAGGATT 481
DB      484 CCATCAACCAAGCTGTGACTGCTGAGGATCCGCTGCTCCGTTATGAGATCAAGGATA 543
QY      482 TGGTTCGCGCGC 493
DB      544 TCCATGTGCCAC 555

RESULT 36
US-10-198-846-13409
; Sequence 13409, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steilmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
```

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; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13409
; LENGTH: 1150
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1149..1150
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-13409

Query Match      11.6%; Score 110; DB 14; Length 1150;
Best Local Similarity 49.4%; Pred. No. 5e-26;
Matches 345; Conservative 0; Mismatches 320; Indels 33; Gaps 1;

QY      218 TCAGCGCGGATTAACGAATTTGACTGTGACGCGATCATTTATTTCCAAAGTACCAGATC 277
DB      127 TGACTCTGACATGTAATCTGCAAAATCGATGAGTCTCTTACCTGCGCATCATGAGCC 186
QY      278 CCAACTCGCTTCATACAGGTTTCGACCACTACATTATGGCAATTAACCAAGTTGCCCAAA 337
DB      187 CTTACAAAGCAAGCTACAGGTGTGAGAGACCTGAGTATGCGTCAACGCTAAGCTCMAA 246
QY      338 CGAGCTGCGTTCCGTTATCGGCGCTATGAGTTGAGCAAAAAGTTTGAAAGACGAGC 397
DB      247 CAACATGATGATCAAGCTTCGGCAAACTCTCTGTGACAAATCTTCGGGAAACGGAGAT 306
QY      398 AATCAACAGTACCGTGTCTCCGCTTCGATGAAGCCGCGGCTTGGGTGTGAAG 457
DB      307 CCTGAATCCAGCATTTGTGATGATGATCAACCAAGCTGCTGATCTGGGGTATCCGCT 366
QY      458 TCTCTCGTTAGCAATTCAGGATTTTGTTCGCGCCCAAGAAATCCGTGCGCAATGACAG 517
DB      367 GCTCTGTTATGATCAAGATATTCATGATCCATGTCACCCCGGTGAAGAGTCTATGACA 426
QY      518 CACAATTAACCGCGCAACGCGAAAGCGCCGCTATTGCGCAATCCGAAGCCGTTAAA 577
DB      427 TCGAGGTGAGCAAGCGCGGAGAAAGCGGCAAGTCTTAAGTCTGA----- 475
QY      578 TCGAAACAATCAACTTGTGCACTGTGACGCTGGAAGCCGAATCCAACATCCGAAGCGC 637
DB      476 -----GGGGAACCGAGAGTCCGCTCATTAATGTGCAAGAGGGA 513
QY      638 AGGCTGAGCTGCGGTCAATGCTTCCATATGCCAGAAATGCCCGGCATCAACCGGCGCA 697
DB      514 AGAAACAGGCCCAAGATCTTGCGCTCCGAAGCAAAAAGCTAAACAGATTAATCAGGCAAG 573
QY      698 AAGGCGAAGCGGAATCCCTGCGCTTGTGTGCGAAGCCCAATCCGAAGCCATCCGTCMAA 757
DB      574 CAGAGAGGCCAGGTGAGTCTTGCGAAGGCCAAGGCTTAAGCTAAGCTATTTCCAAATCC 633
QY      758 TTGCGCGCGCCCTTCAACCAAGGCGGCGAGATGCGGTCAATCTGAAGATTGCGGAAC 817
DB      634 TGGCTGCACTCTGACACAAACATTAATGAGATGACAGACCTTCACTGACTGTGCGAGC 693
QY      818 AATAGTACCGCGGTTCAACATCTTGGCCAAAGAAAGCAATAGCTGATTAATGCGCGCA 877
DB      694 AGTATGTGAGCGCGTTCTCCAAATCGGCAAGAGACTCCAAACATTAATCTACTGCGCTCCA 753
QY      878 ATGTGCGCAATTCGGCAGCTGATTTCTGCGCGGAGT 915
DB      754 ACCCTGCGATGTACCAAGATGTGGCTCAGGCAATG 791

RESULT 37
US-09-815-343-1428
; Sequence 1428, Application US/09815343
```

Patent No. US20010055396A1
; GENERAL INFORMATION:
; APPLICANT: Meagher, Madeleine
; APPLICANT: Xu, Jiangchun
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.504
; CURRENT APPLICATION NUMBER: US/09/815,343
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1428
; LENGTH: 691
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(691)
; OTHER INFORMATION: n = A,T,C or G
US-09-815-343-1428

Query Match 10.2%; Score 96.4; DB 9; Length 691;
Best Local Similarity 52.8%; Pred. No. 1.6e-21;
Matches 208; Conservative 0; Mismatches 186; Indels 0; Gaps 0;

OY 85 GTTGTGAAAGGCTCGGGCGTTTCATCGCCCTGACGGCGGGTTGAAATTTGATT 144
DB 6 GTGTGAGAGCAATGGGCCGATTCACCGGATCTCGAGAGCTGTTTGAACATCTCATC 65
OY 145 CCTTTATGACCGCGTGCCTACCGCAATTCGCTGAAAGAAATCCCTTTAGAGTACC 204
DB 66 CCGTGTGAGAGCAATGGGCCGATTCACCGGATCTCGAGAGCTGTTTGAACATCTCATC 125
OY 205 AGCCAGGCTGATACCGCGGATTAATGCAATGATCTGAGCGCATCATCTTTC 264
DB 126 GAGCAGTGGCTGTACTCTGCAATGATTAATCTGCAAAATGATGAGTCTTTACCTG 185
OY 265 CAAGTAACCGATCCCAACTCGCTCATACGTTGAGCAACTACATTAATGCAATTACC 324
DB 186 CGCATCATGACCTTTACAGGCAAGCTACGTTGAGAGAGCCCTGAGTATCCGCTACC 245
OY 325 CAGCTTGGCCAAACGACGCTGCTTCGTTATCGGGCGTATGAGATTGACAAAACGTTT 384
DB 246 CAGTAGTCAAAACCAACATGATCAAGAGCTCGGCAAACTCTCTGCAAAAGTCTTC 305
OY 385 GAAAGACCGGACGAATCAACATGATCCGTTCTCCGCTTGAAGAGCCGCGGGCT 444
DB 306 CGGAGCGGAGTCCCTGAATGCGCATTTGATGATGATCAACCAAGCTGACTGC 365
OY 445 TGGGGTGTGAAGTCTCGTTACGAATCAAG 478
DB 366 TGGGTATCCGCTCGCTCGTTATGATCAAG 399

RESULT 38

US-10-097-105-1428
; Sequence 1428, Application US/10097105
; Publication No. US20040037842A1
; GENERAL INFORMATION:
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: King, Gordon E.
; APPLICANT: Secrist, Heather
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.504C1
; CURRENT APPLICATION NUMBER: US/10/097,105
; NUMBER OF SEQ ID NOS: 1562
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1428

LENGTH: 691
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 439, 508, 523, 526, 539, 561, 575, 582, 584, 602, 614, 623,
; LOCATION: 626, 645, 648, 664
; OTHER INFORMATION: n = A,T,C or G
US-10-097-105-1428

Query Match 10.2%; Score 96.4; DB 18; Length 691;
Best Local Similarity 52.8%; Pred. No. 1.6e-21;
Matches 208; Conservative 0; Mismatches 186; Indels 0; Gaps 0;

OY 85 GTTGTGAAAGGCTCGGGCGTTTCATCGCCCTGACGGCGGGTTGAAATTTGATT 144
DB 6 GTGTGAGAGCAATGGGCCGATTCACCGGATCTCGAGAGCTGTTTGAACATCTCATC 65
OY 145 CCTTTATGACCGCGTGCCTACCGCAATTCGCTGAAAGAAATCCCTTTAGAGTACC 204
DB 66 CCGTGTGAGAGCAATGGGCCGATTCACCGGATCTCGAGAGCTGTTTGAACATCTCATC 125
OY 205 AGCCAGGCTGATACCGCGGATTAATGCAATGATCTGAGCGCATCATCTTTC 264
DB 126 GAGCAGTGGCTGTACTCTGCAATGATTAATCTGCAAAATGATGAGTCTTTACCTG 185
OY 265 CAAGTAACCGATCCCAACTCGCTCATACGTTGAGCAACTACATTAATGCAATTACC 324
DB 186 CGCATCATGACCTTTACAGGCAAGCTACGTTGAGAGAGCCCTGAGTATCCGCTACC 245
OY 325 CAGCTTGGCCAAACGACGCTGCTTCGTTATCGGGCGTATGAGTTGACAAAACGTTT 384
DB 246 CAGTAGTCAAAACCAACATGATCAAGAGCTCGGCAAACTCTCTGCAAAAGTCTTC 305
OY 385 GAAAGACCGGACGAATCAACATGATCCGTTCTCCGCTTGAAGAGCCGCGGGCT 444
DB 306 CGGAGCGGAGTCCCTGAATGCGCATTTGATGATGATCAACCAAGCTGACTGC 365
OY 445 TGGGGTGTGAAGTCTCGTTACGAATCAAG 478
DB 366 TGGGTATCCGCTCGCTCGTTATGATCAAG 399

RESULT 39

US-09-969-034-3476
; Sequence 3476, Application US/09969034
; Publication No. US20040110668A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Asle, Jon H.
; APPLICANT: Carroll, Eddie III
; APPLICANT: Carino, Theodore J.
; APPLICANT: Dwivedi, Poorvima
; APPLICANT: Molino, Gary A.
; APPLICANT: Thagalingam, Arunthathi
; APPLICANT: Lewis, Marcia E.
; TITLE OF INVENTION: Nucleic Acid Sequences Differentially
; FILE REFERENCE: 1657/1032
; CURRENT APPLICATION NUMBER: US/09/969,034
; PRIOR APPLICATION NUMBER: 60/237,271
; NUMBER OF SEQ ID NOS: 4494
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3476
; LENGTH: 683
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 466, 484, 511, 517, 524, 542, 546, 549, 582, 604, 611, 617,
; LOCATION: 651, 660, 666, 680, 683

OTHER INFORMATION: n = A,T,C or G
US-09-969-034-3476

Query Match 10.1%; Score 95.6; DB 11; Length 683;
Best Local Similarity 53.3%; Pred. No. 3e-21;
Matches 223; Conservative 0; Mismatches 194; Indels 1; Gaps 1;

QY 62 TCATCCCCCAGAGAGAGATCCAGCTTGTGAAAAGGCTCGGGGCTTTCCATCGCCCTTGA 121
DB 9 TCGTCCCGCAGAGAGAGGCTGCGTGTGTGAGCGATGCGCGATTCACCGCATCTGG 68
QY 122 CGGCGGCTTTGAATTTTGAATTCCTTATGACCGCGGTCCGCTTACCGCATTCGCTGA 181
DB 69 ACCCTGCTTGAACATCCATCCATCCCTGTGTGAGCCGATCCGATATGTCAGAGTCTCA 128
QY 182 AAGAAATCCCTTTAAGAGTACCCAGCCAGCTGTCATCAAGCGCGATTAATGCAATTTGA 241
DB 129 AGGAAATTCATCAACGTCGCTGAGCACTCGGCTGTGACTCTCGAATGTAATCTCTGC 188
QY 242 CTGTGACGGCATCATCTTATTTCCAAAGTACCGATCCAACTCGCTCATACGTTTGA 301
DB 189 AATGATGAGATCTCTTACCTGACGATCATGGAACCTTACAAAGCAAGCTACGCTGTG 248
QY 302 GCAATCACTTATGCAATTAACCCAGCTTGCCTCAACGAGCGCTGCGTTATGCGGCG 361
DB 249 AGGACCTGAGTATGCGCTGACCCAGCTGCTCAACCAACATGATGAGAGCTGCGCA 308
QY 362 GTATGAGTTGAGCAAAAGCTTTGAAGAGCGAGCAAAATCAACAGTACGCTGCTCCG 421
DB 309 AACTCTCTGAGCAAAAGCTTCCGGAAAGGAGATCCCTGAATGCAAGATTGTGGATG 368
QY 422 CCTCGATGAGCGCGCGGCTTGGGGTGTGAAGT-CCTCGTTACGAATCAAG 478
DB 369 CCATCAACCAAGCTGTGACTGCTGCGGTATCCGCTGCTCGTTATGAGATCAAG 426

RESULT 40

US-09-998-1161/c
Sequence 1161, Application US/0998598
Patent No: US20020150922A1
GENERAL INFORMATION:
APPLICANT: Stolk, John A.
APPLICANT: Xu, Jiangchun
APPLICANT: Chenault, Ruth A.
APPLICANT: Meagher, Madelein Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.561
CURRENT APPLICATION NUMBER: US/09/998, 598
CURRENT FILING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 2606
SOFTWARE: Corixa Invention Disclosure Database
SEQ ID NO 1161
LENGTH: 622
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 615
OTHER INFORMATION: n = A,T,C or G
US-09-998-598-1161

Query Match 9.7%; Score 91.8; DB 9; Length 622;

Best Local Similarity 48.0%; Pred. No. 5.6e-20;
Matches 258; Conservative 1; Mismatches 278; Indels 0; Gaps 0;

QY 198 CGTACCAGCCAGTCTGATCAAGCGGATTAATGCAATGATGTTGACGGCATCAT 257
DB 614 CGGCGCTGAGCAAGCTGCTGTGACTCTGCAAGATGTAATCTGCAATTCATGATGAGTCT 555
QY 258 CTATTTCCAGTAAAGCATCCAAAGCTCGCTCATACGTTGAGAGCAACTATTTAGC 317
DB 554 TTACCTGCGCATGAGACCTTTACAAAGCAAGCTACGCTGAGAGGACCTTGAATATGC 495

QY 318 AATTACCCAGCTTGCCCAAGAGCGTGCCTTCCGTTATTCGGGCGTATGAGTTGACAA 377
DB 494 CGTACCCAGCTAGCTTCAAAACATCATGATCAGAGCTCGGCAAACTCTCTGTGACAA 435
QY 378 AACGTTGAGAACCGGAGCAAGAAATCAAGTACCGTCTTCGCTCGGCTTGATGAAGCGC 437
DB 434 AGCTTCCGGGAGACGGAGAGTCCCTGTAATGCCAGCATTTGTGATGCTCATCAACCAAGCTGC 375
QY 438 CGGGGCTTGGGCTGTAAGATCTCCGTTAGAAATCAAGATTTGTTGCTCCGCGCAAGA 497
DB 374 TGACTGTGGGGTATCCGCTGCTCCGTTATGAGATCAAGGATATCCATGTGCCACCCCG 315
QY 498 AATCTTGGCGCAATGACAGGCAAAATTAACGCGGAGCGGAAAACGCGCGTATTGC 557
DB 314 GGTGAAGAGTCTATGAGATGACAGTGAAGGAGGAGGCGGAGAACGGCCACAGTTCT 255
QY 558 CGAATCCGAGGCGCTTAATTAATGAAACAAATCAACTTGCAGTGTGACGCTGAAGCGGA 617
DB 254 AGAGTCTGAGGGAGACCGAGAGTCCGCTCATTAATGTGGCAGAGAGGAGAAACAGGCCCA 195
QY 618 AATCCAAATCCGAGGCGAGCTCAGGCTGCGTCAATGCTCCATGCTCGAAGAAAT 677
DB 194 GATCTGGGCTCCGAGAGCAAAAAGCTGAACAGATTAATCAGGAGAGAGGAGCGCAG 135
QY 678 CGCCGCAATCAACGCGCTCAAGGCGGAGCGGAATCCCTGCGCTTGTTCGCGAAGC 734
DB 134 TGCACTTCTGGGAGGAGCGGCTTAAGCTGATGATTCGATCTGCTGACGC 78

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Job time : 784 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 13, 2005, 18:32:50 ; Search time 4375 Seconds
(without alignments)
10499.553 Million cell updates/sec

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Perfect score: 948
Sequence: 1 atggaatttcattcattc.....gcagcaaacgcgaataa 948

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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1: gb_da:*
2: gb_hlg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
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9: gb_pr:*
10: gb_ro:*
11: gb_sta:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	948	100.0	948	1	AF235154 Neisseria
2	948	100.0	948	1	AF235155 Neisseria
3	948	100.0	948	1	AF235156 Neisseria
4	948	100.0	948	6	AX043937 Sequence
5	900	94.9	948	1	AF226511 Neisseria
6	900	94.9	948	1	AF226515 Neisseria
7	896.8	94.6	948	1	AF226513 Neisseria
8	896.8	94.6	948	1	AF226528 Neisseria
9	896.8	94.6	948	1	AF226531 Neisseria
10	896.8	94.6	948	1	AF226536 Neisseria
11	896.8	94.6	948	1	AF226537 Neisseria
12	895.2	94.4	948	1	AF226521 Neisseria
13	895.2	94.4	948	1	AF226523 Neisseria
14	895.2	94.4	948	1	AF226533 Neisseria
15	890.4	93.9	948	1	AF226512 Neisseria
16	890.4	93.9	948	1	AF226527 Neisseria
17	890.4	93.9	948	1	AF226541 Neisseria
18	890.4	93.9	948	6	AX043933 Sequence
19	890.4	93.9	948	6	AX043939 Sequence

c	20	890.4	93.9	331801	1	NMA422491	AL162755 Neisseria
	21	886.6	93.5	951	6	AX043931	AX043931 Sequence
	22	884	93.2	948	1	AF226517	AF226517 Neisseria
	23	884	93.2	948	1	AF226518	AF226518 Neisseria
	24	884	93.2	948	1	AF226539	AF226539 Neisseria
	25	880.8	92.9	948	1	AF226539	AF226539 Neisseria
	26	879.2	92.7	948	1	AF226516	AF226516 Neisseria
	27	879.2	92.7	948	1	AF226516	AF226516 Neisseria
	28	877.6	92.6	948	1	AF226522	AF226522 Neisseria
	29	877.6	92.6	948	1	AF226529	AF226529 Neisseria
	30	877.6	92.6	948	1	AF226530	AF226530 Neisseria
	31	877.6	92.6	948	1	AF226532	AF226532 Neisseria
	32	877.6	92.6	948	1	AF226534	AF226534 Neisseria
	33	877.6	92.6	948	1	AF226540	AF226540 Neisseria
	34	877.6	92.6	948	1	AF226540	AF226540 Neisseria
	35	877.6	92.6	948	6	AX043935	AX043935 Sequence
	36	877.6	92.6	10144	1	AE002470	AE002470 Neisseria
	37	877.6	92.6	349980	6	AX044031	AX044031 Sequence
	38	877.6	92.6	349980	6	AX044032	AX044032 Sequence
	39	876	92.4	948	1	AF226526	AF226526 Neisseria
	40	876	92.4	948	1	AF226525	AF226525 Neisseria
	41	869.6	91.7	948	1	AF226534	AF226534 Neisseria
	42	869.6	91.7	948	1	AF226538	AF226538 Neisseria
	43	824.8	87.0	917	1	AF226520	AF226520 Neisseria
	44	547.2	57.7	600	6	AX043929	AX043929 Sequence
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ALIGNMENTS

RESULT 1	AF235154	948 bp	DNA	linear	BCT 22-MAR-2000
LOCUS	AF235154				
DEFINITION	Neisseria gonorrhoeae strain NG-F62 GNA1220 (gna1220) gene.				
ACCESSION	AF235154				
VERSION	AF235154.1	GI:7274431			
KEYWORDS	complete cds.				
SOURCE	Neisseria gonorrhoeae				
ORGANISM	Neisseria gonorrhoeae				
REFERENCE	1 (bases 1 to 948)				
AUTHORS	Pizza, M., Scariato, V., Masignani, V., Giuliani, M.M., Arico, B., Comanducci, M., Jennings, G.T., Baldi, L., Bartolini, E., Capechi, B., Galeotti, C.L., Iuzzo, E., Manetti, R., Marchetti, E., Mora, M., Nuti, S., Ratti, G., Santini, L., Savino, S., Scarcellini, M., Storni, E., Zuo, P., Brooker, M., Hundt, E., Knapp, B., Blair, E., Mason, T., Tettelin, H., Hood, D.W., Jeffries, A.C., Saunders, N.J., Granoff, D.M., Venter, C., Moxon, E.R., Grandi, G., and Rappuoli, R.				
	Identification of vaccine candidates against serogroup B meningococcus by whole-genome sequencing				
	Science 287 (5459), 1816-1820 (2000)				
TITLE	Neisseria gonorrhoeae				
JOURNAL	Neisseria gonorrhoeae				
MEDLINE	20175756				
PUBMED	10710308				
REFERENCE	2 (bases 1 to 948)				
AUTHORS	Pizza, M., Masignani, V., Comanducci, M., Tettelin, H., and Rappuoli, R.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-FEB-2000) IRIS Immunobiological Research Institute in Siena, Chiron SpA, Via Fiorentina, 1, Siena 53100, Italy				
FEATURES	Location/Qualifiers				
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	/mol_type="genomic DNA"				
	/strain="NG-F62"				
	/db_xref="taxon:485"				
	/note="serogroup: B"				
gene	1..948				
	/gene="gna1220"				
CDS	1..948				
	/gene="gna1220"				
	/note="Genome-derived Neisseria Antigen GNA1220"				

Db	61	GTGATCCCCAGAGAAAGTCCAGCTTGTCGAAAGCTGGGCGTTTCATCGCCCTG	120
Qy	121	ACGGCGGTTTGAATATTTTGTATCCCTTATGACCGGCGCTACCGCATTTGCTG	180
Db	121	ACGGCGGTTTGAATATTTTGTATCCCTTATGACCGGCGCTACCGCATTTGCTG	180
Qy	181	AAAGAAATCCCTTTAGAGTACCCAGCCAGGTGATCAACGGCGGTAATATAGCAATTG	240
Db	181	AAAGAAATCCCTTTAGAGTACCCAGCCAGGTGATCAACGGCGGTAATATAGCAATTG	240
Qy	241	ACTGTGAGCGGATCATCTATTTCAGATPACCATCCCAACTCGGCTCATACGGTTG	300
Db	241	ACTGTGAGCGGATCATCTATTTCAGATPACCATCCCAACTCGGCTCATACGGTTG	300
Qy	301	AGCACTACATTAATGCAATTAACCAAGCTTGCCCAACGACGCTGCGTTTCGTTATCGGG	360
Db	301	AGCACTACATTAATGCAATTAACCAAGCTTGCCCAACGACGCTGCGTTTCGTTATCGGG	360
Qy	361	CGTATGAGTTGGAACAAACGTTTGAAGAACGCGACGAATCAACAGTACCGTCTCTCC	420
Db	361	CGTATGAGTTGGAACAAACGTTTGAAGAACGCGACGAATCAACAGTACCGTCTCTCC	420
Qy	421	GCCTTGATGAAACCGCGCGGCTTGCGGATGAAAGTCTCGTTACGAATCAAGAT	480
Db	421	GCCTTGATGAAACCGCGCGGCTTGCGGATGAAAGTCTCGTTACGAATCAAGAT	480
Qy	481	TTGGTTCCGCGGAGAAATCTTTCGCGCATGACGACCAATTAACCGCGGACGGA	540
Db	481	TTGGTTCCGCGGAGAAATCTTTCGCGCATGACGACCAATTAACCGCGGACGGA	540
Qy	541	AAACGCGCCGATATTCGCGCATGCGAAGCGCTGTAATCAACAACTTTCGCAAT	600
Db	541	AAACGCGCCGATATTCGCGCATGCGAAGCGCTGTAATCAACAACTTTCGCAAT	600
Qy	601	GGTACACGTTGAACCGAAATTCACCAATTCGAAAGCGCTGCGTCAATGCG	660
Db	601	GGTACACGTTGAACCGAAATTCACCAATTCGAAAGCGCTGCGTCAATGCG	660
Qy	661	TCCAAATGCGAGAAATTCGCGCATCAACCGCGCCCAAGCGGAGTCCCTGCGC	720
Db	661	TCCAAATGCGAGAAATTCGCGCATCAACCGCGCCCAAGCGGAGTCCCTGCGC	720
Qy	721	CTTGTTCGCGAAGCCATTCGGAAGCCATTCGTAATTCGCGCGCTTCAAACTCA	780
Db	721	CTTGTTCGCGAAGCCATTCGGAAGCCATTCGTAATTCGCGCGCTTCAAACTCA	780
Qy	781	GGGGGGGCGGATCGGTCAATTCGAAATTCGGAATTCGTAATTCGCGGCTTCAACAT	840
Db	781	GGGGGGGCGGATCGGTCAATTCGAAATTCGGAATTCGTAATTCGCGGCTTCAACAT	840
Qy	841	CTTGCCAAAGAAAGCAATACGCTGATTAATCGCGCATGTTGCCGACATCGGAGCTG	900
Db	841	CTTGCCAAAGAAAGCAATACGCTGATTAATCGCGCATGTTGCCGACATCGGAGCTG	900
Qy	901	ATTTCGCGCGCATGAAATTTATGACAGACGAAACCGCCAAATTA	948
Db	901	ATTTCGCGCGCATGAAATTTATGACAGACGAAACCGCCAAATTA	948

RESULT 3
AF235156 948 bp DNA linear BCT 22-MAR-2000
LOCUS Neisseria gonorrhoeae strain FA1090 GNA1220 (gna1220) gene,
DEFINITION complete cde.
ACCESSION AF235156 GI:7274435
VERSION AF235156.1
KEYWORDS
SOURCE Neisseria gonorrhoeae
ORGANISM Neisseria gonorrhoeae
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.

AUTHORS	Pizza, M., Scarlato, V., Masi, V., Giuliani, M., Arico, B., Comanducci, M., Jennings, G.T., Baldi, L., Bartolini, E., Capocchi, B., Galeotti, C.L., Iuzzi, E., Manetti, R., Marchetti, E., Mora, M., Nuti, S., Ratti, G., Santini, L., Savino, S., Scarselli, M., Scorn, E., Zuo, P., Broeker, M., Hundt, E., Knapp, B., Blair, E., Mason, T., Tettelin, H., Hood, D.W., Jeffries, A.C., Saunders, N.J., Granoff, D.M., Venter, C., Moxon, E.R., Grandi, G., and Rappuoli, R.			
TITLE	Identification of vaccine candidates against serogroup B meningococcus by whole-genome sequencing			
JOURNAL	Science 287 (5459), 1816-1820 (2000)			
MEDLINE	20175756			
REFERENCE	2 (bases 1 to 948)			
AUTHORS	Pizza, M., Masi, V., Comanducci, M., Tettelin, H. and Rappuoli, R.			
JOURNAL	Submitted (16-FEB-2000) IRIS Immunobiological Research Institute in Siena, Chiron Spa, Via Fiorentina, 1, Siena 53100, Italy			
FEATURES	Location/Qualifiers			
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ORIGIN	Query Match 100.0%; Score 948; DB 1; Length 948; Best Local Similarity 100.0%; Pred. NO. 4.5e-214; Indels 0; Gaps 0; Matches 948; Conservative 0; Mismatches 0;			
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 DEFINITION Sequence 16 from Patent WO066791.
 ACCESSION AX043937
 VERSION AX043937.1 GI:11342858

KEYWORDS
 SOURCE
 ORGANISM
 Neisseria gonorrhoeae
 Neisseria gonorrhoeae
 Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 Neisseriaceae; Neisseria.
 REFERENCE
 AUTHORS
 1 Pizze, M., Hickey, E., Peterson, J., Tetrelin, H., Venter, J. C.,
 Massignani, V., Galeotti, C., Mora, M., Ratti, G., Scariello, M.,
 Scarlato, V., Rappunoli, R., Frazer, C. M. and Grandi, G.
 TITLE
 JOURNAL
 Neisseria genomic sequences and methods of their use
 Patent: WO 006791-A 16 09-NOV-2000;
 CHIRON CORPORATION (US); THE INSTITUTE FOR GENOMIC RESEARCH (US)
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 Best local Similarity 100.0%; Pred. No. 4,5e-214;
 Matches 948; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 LOCUS AF226511 948 bp DNA linear BCT 11-MAR-2000
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 ACCESSION AF226511
 VERSION AF226511.1 GI:7228851
 KEYWORDS
 SOURCE
 ORGANISM
 Neisseria meningitidis
 Neisseria meningitidis
 Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 Neisseriaceae; Neisseria.
 REFERENCE
 AUTHORS
 1 (bases 1 to 948)
 Pizze, M., Scarlato, V., Massignani, V., Giuliani, M. M., Arico, B.,

Commanducci, M., Jennings, G.T., Baldi, L., Bartolini, E., Capecechi, B.,
 Galeotti, C.L., Luzzi, B., Manetti, R., Marchetti, E., Mora, M.,
 Nuti, S., Ratti, G., Santini, L., Savino, S., Scarselli, M., Stormi, E.,
 Zuo, P., Brooker, M., Hundt, E., Knapp, B., Blair, E., Mason, T.,
 Tettelin, H., Hood, D.W., Jeffries, A.C., Saunders, N.J., Granoff, D.M.,
 Venter, C., Moxon, E.R., Grandi, G. and Rappuoli, R.
 Identification of vaccine candidates against serogroup B
 meningococcus by whole-genome sequencing
 Science 287 (5459), 1816-1820 (2000)

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 20175756
 10710308
 2 (bases 1 to 948)
 AUTHORS
 Pizzz, M., Masignani, V., Commanducci, M., Tettelin, H. and Rappuoli, R.
 Direct Submission
 Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in
 Siena, Chiron SPA, Via Fiorentina, 1, Siena 53100, Italy
 JOURNAL
 TITLE
 LOCATION/Qualifiers

FEATURES
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ORIGIN
 Query Match 94.9%; Score 900; DB 1; Length 948;
 Best Local Similarity 96.8%; Pred. No. 1,1e-202;
 Matches 918; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

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 ACCESSION
 AF226515
 VERSION
 AF226515.1 GI:7228859
 KEYWORDS
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 Neisseria meningitidis
 Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 Neisseriaceae; Neisseria.
 REFERENCE
 1 (bases 1 to 948)
 Pizzz, M., Scariato, V., Masignani, V., Giuliani, M.M., Arico, B.,
 Commanducci, M., Jennings, G.T., Baldi, L., Bartolini, E., Capecechi, B.,
 Galeotti, C.L., Luzzi, B., Manetti, R., Marchetti, E., Mora, M.,
 Nuti, S., Ratti, G., Santini, L., Savino, S., Scarselli, M., Stormi, E.,
 Zuo, P., Brooker, M., Hundt, E., Knapp, B., Blair, E., Mason, T.,
 Tettelin, H., Hood, D.W., Jeffries, A.C., Saunders, N.J., Granoff, D.M.,
 Venter, C., Moxon, E.R., Grandi, G. and Rappuoli, R.
 Identification of vaccine candidates against serogroup B
 meningococcus by whole-genome sequencing
 Science 287 (5459), 1816-1820 (2000)

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 20175756
 10710308
 2 (bases 1 to 948)
 REFERENCE
 Pizzz, M., Masignani, V., Commanducci, M., Tettelin, H. and Rappuoli, R.
 Direct Submission
 Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in
 Siena, Chiron SPA, Via Fiorentina, 1, Siena 53100, Italy
 JOURNAL
 TITLE
 LOCATION/Qualifiers

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ORIGIN

Query Match 94.9%; Score 900; DB 1; Length 948;
 Best Local Similarity 96.8%; Pred. No. 1.1e-202;
 Matches 918; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

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RESULT 7
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 DEFINITION
 Neisseria meningitidis strain 297-0 membrane protein GNA1220
 (gna1220) gene, complete cds.
 ACCESSION
 AF226513
 VERSION
 AF226513.1 GI:7228865
 KEYWORDS
 SOURCE
 ORGANISM
 Neisseria meningitidis
 Neisseria meningitidis
 Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 Neisseriaceae; Neisseria.

REFERENCE
 AUTHORS
 1 (bases 1 to 948)
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 Comanducci, M., Jennings, G.T., Baldi, L., Bartolini, E., Capecci, B.,
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 Zuo, P., Brooker, M., Hündt, E., Knapp, B., Blair, E., Mason, T.,
 Tettelin, H., Hood, D.W., Jeffries, A.C., Saunders, N.J., Granoff, D.M.,
 Venter, C., Moxon, E.R., Grandi, G. and Rappuoli, R.
 Identification of vaccine candidates against serogroup B
 meningococcus by whole-genome sequencing
 JOURNAL
 MEDICAL
 JOURNAL
 PUBLISHED
 201710308
 10710308
 2 (bases 1 to 948)
 Pizza, M., Masignani, V., Comanducci, M., Tettelin, H. and Rappuoli, R.
 Direct Submission
 Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in
 Siena, Chiron SpA, Via Fiorentina, 1, Siena 53100, Italy
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 LOCUS AF226528
 DEFINITION Neisseria meningitidis strain F6124 membrane protein GNA1220

ACCESSION AF226528
 VERSION AF226528.1
 KEYWORDS Neisseria meningitidis
 SOURCE Neisseria meningitidis
 ORGANISM Neisseria meningitidis
 Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.

REFERENCE 1 (bases 1 to 948)
 Pizzo, M., Scariato, V., Masignani, V., Giuliani, M.M., Arico, B., Comanducci, M., Jennings, G.T., Baldi, L., Bartolini, E., Capecechi, B., Galeotti, C.L., Iuzzi, E., Manetti, R., Marchetti, E., Mora, M., Nuti, S., Ratti, G., Santini, L., Savino, S., Scarcellini, M., Scorni, E., Zuo, P., Broeker, M., Hunds, E., Knapp, B., Blair, E., Mason, T., Tettelin, H., Hood, D.W., Jeffries, A.C., Saunders, N.J., Granoff, D.M., Venter, C., Moxon, E.R., Grandi, G., and Rappelli, R.
 Identification of vaccine candidates against serogroup B meningococcus by whole-genome sequencing
 Science 287 (5459), 1816-1820 (2000)

TITLE JOURNAL MEDLINE
 PUBMED 10710308
 REFERENCES Pizzo, M., Masignani, V., Comanducci, M., Tettelin, H. and Rappelli, R.
 Direct Submission
 Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in Siena, Chiron Spa, Via Fiorentina, 1, Siena 53100, Italy

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DEFINITION (gna1220) gene, complete cds.
ACCESSION AF226531
VERSION AF226531.1 GI:7228890
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SOURCE Neisseria meningitidis
ORGANISM Neisseria meningitidis; Betaproteobacteria; Neisseriales;
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REFERENCE 1 (bases 1 to 948)
AUTHORS Pizzo, M., Scarlato, V., Maignani, V., Giuliani, M.M., Arico, B.,
Comanducci, M., Jennings, G.T., Baldi, L., Bartolini, E., Capechi, B.,
Galeotti, C.L., Luzzi, E., Manetti, R., Marchetti, B., Mora, M.,
Nuti, S., Ratti, G., Santini, L., Savino, S., Scarselli, M., Stormi, E.,
Zuo, P., Brooker, M., Hundt, E., Knapp, B., Blair, E., Mason, T.,
Tettelin, H., Hood, D.W., Jeffries, A.C., Saunders, N.J., Granoff, D.M.,
Venter, C., Moxon, E.R., Grandi, G. and Rappuoli, R.
Identification of vaccine candidates against serogroup B
meningococcus by whole-genome sequencing
Journal Science 287 (5459), 1816-1820 (2000)
MEDLINE 20175756
PUBMED 10710308

REFERENCE 2 (bases 1 to 948)
AUTHORS Pizzo, M., Maignani, V., Comanducci, M., Tettelin, H. and Rappuoli, R.
TITLE Direct Submission
JOURNAL Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in
Stena, Chiron Spa, Via Fiorentina, 1, Stena 53100, Italy
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Query Match 94.6%; Score 896.8; DB 1; Length 948;
Best Local Similarity 96.6%; Pred. No. 6.3e-202;
Matches 916; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
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LOCUS AF26536

DEFINITION (gna1220) gene, complete cds.

ACCESSION AF26536

VERSION AF26536.1 GI:7228900

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 948)

Pizza, M., Scarlato, V., Masi, V., Giuliani, M.M., Arico, B., Comanducci, M., Jennings, G.T., Baldi, L., Bartoloni, E., Capocchi, B., Galeotti, C.L., Luzzi, B., Manetti, R., Marchetti, R., More, M., Nuti, S., Ratti, G., Santini, L., Savino, S., Scarselli, M., Stormi, E., Zuo, P., Broeker, M., Hunds, E., Knapp, B., Blair, E., Mason, T., Tettelin, H., Hood, D.W., Jeffries, A.C., Saunders, N.J., Granoff, D.M., Venter, C., Moxon, E.R., Grandi, G. and Rappuoli, R.

Identification of vaccine candidates against serogroup B meningococcus by whole-genome sequencing

Science 287 (5459), 1816-1820 (2000)

TITLE

JOURNAL

MEDLINE

PUBMED

2 (bases 1 to 948)

Pizza, M., Masi, V., Comanducci, M., Tettelin, H. and Rappuoli, R.

Direct Submision

Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in Siena, Chiron SPA, Via Fiorentina, 1, Siena 53100, Italy

JOURNAL

FEATURES

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RESULT 11
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DEFINITION *Neisseria meningitidis* strain NGH6 membrane protein GNA1220
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ACCESSION AF226537
VERSION AF226537.1 GI:7228902
KEYWORDS
SOURCE *Neisseria meningitidis*
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Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
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1 (bases 1 to 948)
Piazza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
Galeotti C.L., Luzzi E., Manetti R., Marchetti B., Mora M.,
Nuti S., Ratti G., Santini L., Savino S., Scarselli M., Stormi E.,
Zuo P., Brooker M., Hundt E., Knapp B., Blair E., Mason T.,
Tetelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M.,
Venter C., Moxon E.R., Grandi G. and Rappuoli R.
Identification of vaccine candidates against serogroup B
meningococcus by whole-genome sequencing
Science 287 (5459), 1816-1820 (2000)

TITLE
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MEDLINE
PUBMED
REFERENCE
AUTHORS
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JOURNAL
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DEFINITION *Neisseria meningitidis* strain B2147 gna1220 gene, complete
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ACCESSION AF226521
VERSION AF226521.1 GI:7228970
KEYWORDS
SOURCE *Neisseria meningitidis*
ORGANISM *Neisseria meningitidis*
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
REFERENCE
1 (bases 1 to 948)
Piazza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,

Comanducci, M., Jennings, G.T., Baldi, L., Bartolini, E., Capecci, B., Galeotti, C.L., Luzzi, B., Manetti, R., Marchetti, E., Mora, M., Nuti, S., Ratti, G., Santini, L., Savino, S., Scarselli, M., Storni, E., Zuo, P., Broeker, M., Hundt, E., Knapp, B., Blair, E., Mason, T., Tettelin, H., Hood, D.W., Jeffries, A.C., Saunders, N.J., Granoff, D.M., Venter, C., Moxon, E.R., Grandi, G., and Rappuoli, R.
Identification of vaccine candidates against serogroup B meningococcus by whole-genome sequencing
Science 287 (5459), 1816-1820 (2000)

JOURNAL MEDLINE 2 (bases 1 to 948)
PUBMED 10710308

REFERENCE Pizza, M., Masiugnani, V., Comanducci, M., Tettelin, H. and Rappuoli, R.
Direct Submision Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in Siena, Chiron Spa, Via Fiorentina, 1, Siena 53100, Italy

JOURNAL TITLE Location/Qualifiers

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Query Match 94.4%; Score 895.2; DB 1; Length 948;
Best Local Similarity 96.5%; Pred. No. 1.5e-201;
Matches 915; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

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ACCESSION AF226523
VERSION AF226523.1 GI:7228974
KEYWORDS Neisseria meningitidis
SOURCE Neisseria meningitidis
ORGANISM Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.
REFERENCE 1 (bases 1 to 948)
Pizza, M., Scariato, V., Masiugnani, V., Giuliani, M.M., Arico, B., Comanducci, M., Jennings, G.T., Baldi, L., Bartolini, E., Capecci, B., Galeotti, C.L., Luzzi, B., Manetti, R., Marchetti, E., Mora, M., Nuti, S., Ratti, G., Santini, L., Savino, S., Scarselli, M., Storni, E., Zuo, P., Broeker, M., Hundt, E., Knapp, B., Blair, E., Mason, T., Tettelin, H., Hood, D.W., Jeffries, A.C., Saunders, N.J., Granoff, D.M., Venter, C., Moxon, E.R., Grandi, G., and Rappuoli, R.
Identification of vaccine candidates against serogroup B meningococcus by whole-genome sequencing
Science 287 (5459), 1816-1820 (2000)

JOURNAL MEDLINE 2 (bases 1 to 948)
PUBMED 10710308

REFERENCE Pizza, M., Masiugnani, V., Comanducci, M., Tettelin, H. and Rappuoli, R.
Direct Submision Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in Siena, Chiron Spa, Via Fiorentina, 1, Siena 53100, Italy

JOURNAL TITLE Location/Qualifiers

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(gna1220) gene, complete cds.
ACCESSION
AF226533
VERSION
AF226533.1 GI:7228894
KEYWORDS
SOURCE
ORGANISM
Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
REFERENCE
1 (bases 1 to 948)
Piazza, M., Scarlato, V., Masignani, V., Giuliani, M.M., Arico, B.,
Comanducci, M., Jennings, G.T., Baldi, L., Bartoloni, E., Capecechi, B.,
Galeotti, C.L., Luzzi, E., Manetti, R., Marchetti, E., Mora, M.,
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Zuo, P., Broecker, M., Hundt, E., Knapp, B., Blair, E., Mason, T.,
Tetzelin, H., Hood, E.R., Jelliffe, A.C., Saunders, N.J., Granoff, D.M.,
Venter, C., Moxon, E.R., Grandi, G. and Rappuoli, R.
Identification of vaccine candidates against serogroup B
Meningococcus by whole-genome sequencing
Science 287 (5459), 1816-1820 (2000)
2 (bases 1 to 948)
Piazza, M., Masignani, V., Comanducci, M., Tetzelin, H. and Rappuoli, R.
Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in
Siena, Chiron SpA, Via Fiorentina, 1, Siena 53100, Italy
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Query Match 94.4%; Score 895.2; DB 1; Length 948;
 Best Local Similarity 96.5%; Pred. No. 1.5e-201;
 Matches 915; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

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 LOCUS AF226512
 DEFINITION Neisseria meningitidis strain 205900 membrane protein GNA1220

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 AF226512
 AF226512.1 GI:7228853
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 SOURCE
 ORGANISM
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 Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 Neisseriaceae; Neisseria.
 1 (bases 1 to 948)
 AUTHORS
 Pizzia, M., Scarlato, V., Maignani, V., Giuliani, M.M., Arico, B.,
 Comanducci, M., Jennings, G.T., Baldi, L., Bartolini, E., Capocchi, B.,
 Galeotti, C.L., Iuzzo, E., Manetti, R., Marchetti, E., Mora, M.,
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 Tettelin, H., Hood, D.W., Jeffries, A.C., Sandere, N.J., Granoff, D.M.,
 Venter, C., Moxon, E.R., Grandi, G. and Rappuoli, R.
 Identification of vaccine candidates against serogroup B
 meningococcus by whole-genome sequencing
 Science 287 (5459), 1816-1820 (2000)
 JOURNAL
 MEDLINE
 PubMed
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 2 (bases 1 to 948)
 Pizzia, M., Maignani, V., Comanducci, M., Tettelin, H. and Rappuoli, R.
 Direct Submission
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 Siena, Chiron Spa, Via Fiorentina, 1, Siena 53100, Italy
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 Query Match 93.9%; Score 890.4; DB 1; Length 948;
 Best Local Similarity 96.2%; Pred. No. 2.1e-200;
 Matches 912; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

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RESULT 16
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DEFINITION Neisseria meningitidis strain E32 membrane protein GNA1220
ACCESSION AF226527
VERSION AF226527.1 GI:7228882
KEYWORDS
SOURCE
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REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED

REFERENCE 2 (bases 1 to 948)
AUTHORS Piza, M., Masignani, V., Comanducci, M., Tettelin, H., and Rappuoli, R.
TITLE Direct Submission
JOURNAL Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in
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ORIGIN
Query Match 93.9%; Score 890.4; DB 1; Length 948;
Best Local Similarity 96.2%; Pred. No. 2.1e-200;
Matches 912; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
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LOCUS Neisseria meningitidis strain Z2491 membrane protein GNA1220
DEFINITION (gnal1220) gene, complete cds.
ACCESSION AF226541 GI:7228910
VERSION AF226541
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Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
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Comanducci, M., Jennings, G.T., Baldi, L., Bartolini, E., Capecechi, B.,
Caleo, C.L., Luzzi, E., Manetti, R., Marchetti, E., Mora, M.,
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Zuo, P., Broeker, M., Hunte, E., Knapp, B., Blair, E., Mason, T.,
Tettelin, H., Hood, D.W., Jeffries, A.C., Saunders, N.J., Granoff, D.M.,
Venter, C., Moxon, B.R., Grand, G. and Rappuoli, R.
Identification of vaccine candidates against serogroup B
meningococcus by whole-genome sequencing
Science 287 (5459), 1816-1820 (2000)

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MEDLINE
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VERSION AX043933.1 GI:11342856
KEYWORDS
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Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
REFERENCE
AUTHORS
1 Pizzo, M., Hickey, E., Peterson, J., Tettelin, H., Venter, J.C.,
Masignani, V., Galeotti, C., Mora, M., Ratti, G., Scarselli, M.,
Scarlato, V., Rappuoli, R., Frazer, C.M. and Grandi, G.,
Neisseria genomic sequences and methods of their use
Patent: WO 0066791-A 12 09-NOV-2000;
JOURNAL
CHIRON CORPORATION (US) ; THE INSTITUTE FOR GENOMIC RESEARCH (US)
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Query Match 93.9%; Score 890.4; DB 6; Length 948;
Best Local Similarity 96.2%; Pred. No. 2.1e-200;
Matches 912; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

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DEFINITION Sequence 18 from Patent WO0066791.
ACCESSION AX043939
VERSION AX043939.1 GI:11342859
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Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
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AUTHORS
1 Pizzo, M., Hickey, E., Peterson, J., Tettelin, H., Venter, J.C.,
Masignani, V., Galeotti, C., Mora, M., Ratti, G., Scarselli, M.,
Scarlato, V., Rappuoli, R., Frazer, C.M. and Grandi, G.,
Neisseria genomic sequences and methods of their use
Patent: WO 0066791-A 18 09-NOV-2000;
JOURNAL
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ORIGIN
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Best Local Similarity 96.2%; Pred. No. 2.1e-200;
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Db      241 |ACGTGACGGGTATCATCTATTTCCAGTAAACGACCCCAAACTCGCTCATACGGTTGC 300
Qy      301 |AGCAACTACATTAATGGCAATTACCCAGCTTCCCAACGACGCTGCTTCGTTATCGGG 360
Db      301 |AGCAACTACATTAATGGCAATTACCCAGCTTCCCAACGACGCTGCTTCGTTATCGGG 360
Qy      361 |CGTATGAGATTGACAAACAGTTTGAAAGAACGCGACCAATTCACAGTACCGTCTCC 420
Db      361 |CGTATGAGATTGACAAACAGTTTGAAAGAACGCGACCAATTCACAGTACCGTCTCC 420
Qy      421 |GCCCTGATGAGACCGCGGGGCTTGGGGTGTGAAAGTCTCCGCTACGAATCAAGAT 480
Db      421 |GCCCTGATGAGACCGCGGGGCTTGGGGTGTGAAAGTCTCCGCTACGAATTAAGAC 480
Qy      481 |TTGGTTCCGCGCGCAAGAAATCTTTGCGCAATGACGCAACAAATTACCGCGGAA 540
Db      481 |TTGGTTCCGCGCGCAAGAAATCTTTGCGCAATGACGCGCAACAAATTACCGCGGAA 540
Qy      541 |AAACGCGCCGCTATTCGCGAATCCGAAGCCGCTTAAATCGAACAAATCAACTTGCAGT 600
Db      541 |AAACGCGCCGCTATTCGCGAATCCGAAGGTCGTAAATCGAACAAATCAACTTGCAGT 600
Qy      601 |GGTACGGGTGAGCCGAAATCCCAACATCCGAAGCGAGGCTCAAGCTCGGTCATATCG 660
Db      601 |GGTACGGGTGAGCCGAAATCCCAACATCCGAAGCGAGGCTCAAGCTCGGTCATATCG 660
Qy      661 |TCCATCCCGAAGAAATCGCCCGCATCAACCGCGCAAGCGCAAGCGAATCCCTGCGC 720
Db      661 |TCAATTCGCGAAGAAATCGCCCGCATCAACCGCGCAAGCGCAAGCGAATCCCTGCGC 720
Qy      721 |CTTGTTCCCGAAGCAATTCGCGAAGCGCAATTCGCGCGCTTCAAAACCA 780
Db      721 |CTTGTTCCCGAAGCAATTCGCGAAGCGCAATTCGCGCGCTTCAAAACCA 780
Qy      781 |GGGGGGGCGGATGGGTCATCTGAGATTGGGAGCAATACGTAAGCGGCTTCAACAT 840
Db      781 |GGGGGGGCGGATGGGTCATCTGAGATTGGGAGCAATACGTAAGCGGCTTCAACAT 840
Qy      841 |CTTGCCCAAGAAAGCAATACGCTGATTATGCGCCCAATGTTGCCGATCGCGAGCTG 900
Db      841 |CTTGCCCAAGAAAGCAATACGCTGATTATGCGCCCAATGTTGCCGATCGCGAGCTG 900
Qy      901 |ATTTCGCGCGCATGAAATATTATGACAGCAGCAAAACCGCAATTA 948
Db      901 |ATTTCGCGCGCATGAAATATTATGACAGCAGCAAAACCGCAATTA 948

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RESULT 20
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LOCUS      N18seria meningitidis serogroup A strain 22491 complete genome;
DEFINITION segment 4/7.
ACCESSION AL162755 AL157959
VERSION    AL162755.2 GI:7379742
KEYWORDS
SOURCE
ORGANISM   Neisseria meningitidis 22491
            Neisseria meningitidis 22491
            Bacteria: Proteobacteria; Betaproteobacteria; Neisseriales;
            Neisseriaceae; Neisseria.
REFERENCE 1 (bases 1 to 331801)
AUTHORS   Parkhill,J., Achtman,M., James,K.D., Bentley,S.D., Churcher,C.,
            Klee,S.R., Morelli,G., Baaham,D., Brown,D., Chillingworth,T.,
            Davies,R.M., Davis,P., Devlin,K., Felwell,T., Hamlin,N.,
            Holtroff,S., Jagsels,K., Leather,S., Moule,S., Mungall,K.,
            Quail,M.A., Rajandream,M.A., Rutherford,K.M., Simmonds,M.,
            Skelton,V., Whitehead,S., Spratt,B.G. and Barrall,B.G.
TITLE      Complete DNA sequence of a serogroup A strain of Neisseria
            meningitidis 22491
JOURNAL    Nature 404 (6777), 502-506 (2000)
MEDLINE    20222556
PUBMED     10761919
REFERENCE 2 (bases 1 to 331801)

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AUTHORS   Parkhill,J.
TITLE      Direct Submission
JOURNAL    Submitted (30-MAR-2000) Submitted on behalf of the Neisseria
            sequencing team, Sanger Centre, Wellcome Trust Genome Campus,
            Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk
COMMENT    Notes:
            Details of N. meningitidis sequencing at the Sanger Centre are
            available on the World Wide Web.
            (URL, http://www.sanger.ac.uk/Projects/N\_meningitidis/).
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FEATURES

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/organism="Neisseria meningitidis 22491"

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/db_xref="taxon:122587"

/note="serogroup: A"

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/pseudo

117..1333

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/transl_table=11

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/complement(157..166)

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/label=DUS

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/gene="NMA1040"

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/pseudo

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CDS

misc_feature

repeat_region

misc_feature

misc_feature

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restriction-modification system restriction protein, len:
291 aa; similar to parts of many e.g. SW:R1R1.ECOLI
(EMBL:X13145), hsdR, Escherichia coli type I restriction
enzyme EcoRI2411 R protein (EC 3.1.21.3) (1033 aa), fasta
scores; E(): 0, 73.9% identity in 291 aa overlap (frame
1), followed by a stop codon, E(): 0, 92.9% identity in
127 aa overlap (frame 1), followed by a frameshift near a
poly-A tract, E(): 0, 72.5% identity in 604 aa overlap
(frame 3)"
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complement(4559..6838)
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/note="NMA1045, c1pA, probable ATP-dependent protease
ATP-binding protein, len: 759 aa; similar to many e.g.
SW:CLPA.ECOLI (EMBL:M31045), c1pA, Escherichia coli
ATP-dependent Clp protease ATP-binding subunit (758 aa),
fasta scores; E(): 0, 56.2% identity in 762 aa overlap.
Similar to NMA1683, fasta scores; E(): 0, 37.2% identity
in 844 aa overlap. Contains Pfam match to entry PF00495
c1pA/B, Chaperonin c1pA/B, P800871 Chaperonins c1pA/B
signature 1, P800871 Chaperonins c1pA/B signature 2 and
two P800017 ATP/GTP-binding site motif A (P-loop)"
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KIPHALIPIDETHTTIGASTSGCTMDANLKPALAKALCIGATTYDERTYEDK
DHLSRFQKIDIVEPTVSEVQILKGLPMFEGHQAIVTQGLAEAALESARTINE
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Query Match 93.9%; Score 890.4; DB 1; Length 331801;
Best Local Similarity 96.2%; Pred. No. 2,5e-200;
Matches 912; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
QY 1 ATGGAATTTTCATTATCTTGTGGACGCGTTCGCGTTTGCGCTTCAATCCTTTGTC 60
DB 285525 ATGGAATTTTCATTATCTTGTGGACGCGTTCGCGTTTGCGCTTCAATCCTTTGTT 285466
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DB 285465 GTCAATCCCCGACAGGAAGTCCAGCTTCGAAAGGCTCGGGCGTTTCATCGGCGCCCTG 285406
QY 121 ACGGCGGTTTGAATTTTGAATTCCTTTATCGACGCGTTCGCTTACCGCATTCGCTG 180
DB 285405 ACGGCGGTTTGAATTTTGAATTCCTTTATCGACGCGTTCGCTTACCGCATTCGCTG 285346
QY 181 AAAGAAATCCCTTTAGACGTACCCAGCAAGCTCTGCATCAGCGGATATACCAATTG 240
DB 285345 AAAGAAATCCCTTTAGACGTACCCAGCAAGCTCTGCATCAGCGGATATACCAATTG 285286
QY 241 ACTGTTGACGCGATCATCTATTTCCAAAGTACCGATCCCAATCGCTCATAGGTTTCG 300
DB 285285 ACTGTTGACGCGATCATCTATTTCCAAAGTACCGATCCCAATCGCTCATAGGTTTCG 285226
QY 301 AGCACTACATTTATGCAATTTACCGAGCTTGCCCAAGCAAGCAAGCTGCTGCTTATCGGG 360
DB 285225 AGCACTACATTTATGCAATTTACCGAGCTTGCCCAAGCAAGCAAGCTGCTGCTTATCGGG 285166
QY 361 CGTATGAGTGTGACAAACGTTTGAAGACGCGAAGAAATCAACAGTACGCTCTTC 420
DB 285165 CGTATGAGTGTGACAAACGTTTGAAGACGCGAAGAAATCAACAGTACGCTCTTC 285106
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DB 285105 GCCCTCGATGAAGCCGCGCGGCTTGCGGTGTGAAGTCCCTCCGTTAGAAATCAAGAT 285046
QY 481 TTGGTTCCGCGCAAGAAATCCTTGCGCGATGACGACCAATTAACGCGCAAGCGGAA 540
DB 285045 TTGGTTCCGCGCAAGAAATCCTTGCGCGATGACGCGCAATTAACGCGGAA 284986
QY 541 AAACGCGCGCGTATTTGCGGAATCGAAGCGCGTAAATCGAACAATCAACTTGCAGT 600
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 Db 284925 GGTCAACGCGGAAGCCGAAATCCAAATCGAAGGAGGCTCGAGCTGGCTCAATGCG 284866
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 Db 284865 TCATAATGCGAAGAAATCGCCGCAATCAACCGCGCAAGGCGAATCCCTGGCG 284806
 Qy 721 CTGTGTCGGAAGCCCAATCGCCGCAATCGCTCAATGCGCGCCCTTCAACCCAA 780
 Db 284805 CTGTGTCGGAAGCCCAATCGCCGCAATCGCTCAATGCGCGCCCTTCAACCCAA 284746
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 Qy 841 CTGCGCAAGAAAGCAATACGCTGATTTATGCGCCCAATGTCGCAATCGGAGCTG 900
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RESULT 21
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 DEFINITION AX043931
 ACCESSION AX043931
 VERSION AX043931.1 GI:11342855
 KEYWORDS
 SOURCE Neisseria gonorrhoeae
 ORGANISM Neisseria gonorrhoeae
 Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 Neisseriaceae; Neisseria.
 REFERENCE
 AUTHORS 1
 TITLE Piazza, M., Hickey, E., Peterson, J., Tetzelin, H., Venter, J.C.,
 Masignani, V., Galeotti, C., Mora, M., Ratti, G., Scarcellì, M.,
 Scarlato, V., Rappunli, R., Frazer, C.M., and Grandi, G.
 Neisseria genomic sequences and methods of their use
 Patent: WO 006791-A 10 09-NOV-2000;
 JOURNAL CHIRON CORPORATION (US); THE INSTITUTE FOR GENOMIC RESEARCH (US)
 FEATURES
 Source 1..951
 location/Qualifiers
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 Best Local Similarity 96.7%; Pred. No. 1,7e-199;
 Matches 916; Conservative 0; Mismatches 29; Indels 2; Gaps 1;

Qy 1 ATGGAATTTTCAATTATCTGTTGGGAGCGCTGCGCTTTGCGCTCAATCTTGTG 60
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 Qy 181 AAAAGAAATCCCTTGAAGATGACGAGGCTGATCGACGCGCGATTAATACCAATG 240
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Qy 241 ACTGTGACGGCATCATCTATTTCAGTAACCGATCCCAATCGCTCATACGGTTG 300
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 Db 841 CTGCGCAAGAAAGCAATACGCTGATTTATGCGCCCAATGTCGCAATCGGAGCTG 900
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RESULT 22
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 (gna1220) gene, complete cds.
 ACCESSION AF226517
 VERSION AF226517.1 GI:7228863
 KEYWORDS
 SOURCE Neisseria meningitidis
 ORGANISM Neisseria meningitidis
 Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 Neisseriaceae; Neisseria.
 REFERENCE
 AUTHORS 1 (bases 1 to 948)
 Masignani, V., Giuliani, M.M., Arico, B.,
 Comanducci, M., Jennings, G.T., Baldi, L., Bartoloni, E., Capecechi, B.,
 Galeotti, C.L., Iuzi, E., Manetti, R., Marchetti, E., Mora, M.,
 Nuti, S., Ratti, G., Santini, L., Savino, S., Scarcellì, M., Stormi, E.,
 Zuo, P., Broeker, M., Hunte, E., Krapp, B., Blair, E., Mason, T.,
 Tetzelin, H., Hood, D.W., Jeffries, A.C., Saunders, N.J., Granoff, D.M.,
 Venter, C., Moxon, E.R., Grandi, G., and Rappunli, R.
 Identification of vaccine candidates against serogroup B
 meningococcus by whole-genome sequencing
 Science 287 (5459), 1816-1820 (2000)
 JOURNAL MEDLINE
 20175756

PUBMED 10710308
 REFERENCE 2 (bases 1 to 948)
 AUTHORS Pizze,M., Masignani,V., Comanducci,M., Tettelin,H. and Rappunli,R.
 TITLE Direct Submission
 JOURNAL Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in
 Siena, Chiron SpA, Via Fiorentina, 1, Siena 53100, Italy
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 Best Local Similarity 95.8%; Pred. No. 6.8e-199;
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 DEFINITION Neisseria meningitidis strain 93/4286 membrane protein GNA1220
 ACCESSION (gna1220) gene, complete cds.
 VERSION AF226518
 KEYWORDS AF226518.1 GI:7228865
 SOURCE
 ORGANISM
 Neisseria meningitidis
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 Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 Neisseriaceae; Neisseria.
 REFERENCE
 AUTHORS
 1 (bases 1 to 948)
 Pizze,M., Scarlato,V., Masignani,V., Giuliani,M.M., Arico',B.,
 Comanducci,M., Jennings,G.T., Baldi,L., Bartolini,E., Capecechi,B.,
 Galeotti,C.L., Iuzzi,E., Manetti,R., Marchetti,E., Mora,M.,
 Nuti,S., Ratti,G., Santini,L., Savino,S., Scarselli,M., Storni,E.,
 Zuo,P., Broeker,M., Hündt,E., Knapp,B., Blatr,E., Mason,T.,
 Tettelin,H., Hood,D.W., Jeffries,A.C., Saunders,N.J., Granoff,D.M.,
 Venter,C., Moxon,E.R., Grandi,G. and Rappunli,R.
 Identification of vaccine candidates against serogroup B
 meningococcus by whole-genome sequencing
 JOURNAL
 MEDLINE
 2017556
 10710308
 REFERENCE 2 (bases 1 to 948)
 AUTHORS Pizze,M., Masignani,V., Comanducci,M., Tettelin,H. and Rappunli,R.
 TITLE Direct Submission
 JOURNAL Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in
 Siena, Chiron SpA, Via Fiorentina, 1, Siena 53100, Italy
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AF226539 948 bp DNA linear BCT 11-MAR-2000
 Neisseria meningitidis strain NG165 membrane protein GNA1220

AF226539
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 AF226539.1 GI:7228906

KEYWORDS
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 Neisseria meningitidis
 Neisseria meningitidis
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REFERENCE

1 (bases 1 to 948)
 Pizza, M., Scarlato, V., Masignani, V., Giuliani, M.M., Arico, B.,
 Comanducci, M., Jennings, G.T., Baldi, L., Bartoloni, E., Capecci, B.,
 Galeotti, C.L., Luzzi, E., Manetti, R., Marchetti, B., Mora, M.,
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 Tettelin, H., Hood, D.W., Jeffries, A.C., Saunders, N.J., Granoff, D.M.,
 Venter, C., Moxon, E.R., Grandi, G. and Rappuoli, R.
 Identification of vaccine candidates against serogroup B
 meningococcus by whole-genome sequencing
 Science 287 (5459), 1816-1820 (2000)

JOURNAL

2 (bases 1 to 948)
 Pizza, M., Masignani, V., Comanducci, M., Tettelin, H. and Rappuoli, R.
 Direct Submission
 Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in
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Query Match 93.2%; Score 884; DB 1; Length 948;
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 Matches 908; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

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VERSION AF226519.1
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REFERENCE 1 (bases 1 to 948)
Pizza, M., Scarlato, V., Masignani, V., Giuliani, M.M., Arico, B.,

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Identification of vaccine candidates against serogroup B meningococcus by whole-genome sequencing
Science 287 (5459), 1816-1820 (2000)
JOURNAL
MEDLINE
PUBMED
10710308
2 (bases 1 to 948)
REFERENCE
Pizza, M., Masignani, V., Commanducci, M., Tettelin, H. and Rappuoli, R.
Direct Submission
Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in Siena, Chiron SpA, Via Fiorentina, 1, Siena 53100, Italy
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 Venter, C., Moxon, B.R., Grandi, G. and Rappuoli, R.
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 meningococcus by whole-genome sequencing
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 Direct Submission
 Submitted (19-JUN-2000) IRIS Immunobiological Research Institute in
 Siena, Chiron SpA, Via Fiorentina, 1, Siena 53100, Italy
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QY	721	CTTTGTTGCCGAAGCCAAATCGCAGCAATCGCGCAATTTGCCCGCCCTTTCAAAACCCA	780
Db	721	CTTTGTTGCCGAAGCCAAATCGCAGCAATCGCGCAATTTGCCCGCCCTTTCAAAACCCA	780
QY	781	GGCGGGGGCGATGCGGTCAATCTGAAGATTTGGCGAAACAATACGACCGCGTTCAACAT	840
Db	781	GGCGGGGGCGATGCGGTCAATCTGAAGATTTGGCGAAACAATACGACCGCGTTCAACAT	840
QY	841	CTTGCCAAAGAAAGCAATACGCTGATTTATGCCCCCAATTTGGCCGACATCGGACGCTG	900
Db	841	CTTGCCAAAGAAAGCAATACGCTGATTTATGCCCCCAATTTGGCCGACATCGGACGCTG	900
QY	901	ATTTTCGCGCGATGAAATTTATCGACAGCAAGAAACCGCCAAATTA	948
Db	901	ATTTTCGCGCGATGAAATTTATCGACAGCAAGAAACCGCCAAATTA	948
RESULT 27			
LOCUS	AF226516	948 bp	DNA linear BCT 11-MAR-2000
DEFINITION	Neisseria meningitidis strain 860800 membrane protein GNA1220		
ACCESSION	AF226516		
VERSION	AF226516.1 GI:7228861		
KEYWORDS	Neisseria meningitidis		
SOURCE	Neisseria meningitidis		
ORGANISM	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.		
REFERENCE	1 (bases 1 to 948)		
AUTHORS	Piazza, M., Scarlato, V., Masignani, V., Giuliani, M.M., Arico, B., Comanducci, M., Jennings, G.T., Baldi, L., Barolini, E., Capocchi, B., Galocci, C.L., Luzzi, E., Manetti, R., Marchetti, B., Mora, M., Nuti, S., Ratti, G., Santini, L., Savino, S., Scarselli, M., Storni, E., Zuo, P., Broecker, M., Hundt, E., Knapp, B., Blair, E., Mason, T., Tettelin, H., Hood, D.W., Jeffries, A.C., Saunders, N.J., Granoff, D.M., Venter, C., Moxon, E.R., Grandi, G. and Rappuoli, R.		
	Identification of vaccine candidates against serogroup B meningococcus by whole-genome sequencing		
	Science 287 (5459), 1816-1820 (2000)		
TITLE	1. (bases 1 to 948)		
JOURNAL	Piazza, M., Masignani, V., Comanducci, M., Tettelin, H. and Rappuoli, R.		
MEDLINE	Direct Submision		
PUBMED	Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in		
REFERENCES	Sienna, Chiron Spa, Via Fiorentina, 1, Sienna 53100, Italy		
AUTHORS	Location/Qualifiers		
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CDS	1. .948		
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	LVPPQILRSWQQTTRERKRIAESGRKIBQINLASGQREAITQOSEBAQNAV		
	NASNAKRIARINAKGEASLRIVAEANFAIRQIAALQTOGADAVNLKIAEQYVA		
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ORIGIN			

Query Match			
Best Local Similarity 92.7%; Score 879.2; DB 1; Length 948;			
Matches 905; Conservative 0; Mismatches 43; Indels 0; Gaps 0;			
QY	1	ATGGAATTTTCATTTATCTTTGTTGGACGCGTTCGCGTTTTCGCTTCAATCCCTTGTG	60
Db	1	ATGGAATTTTCATTTATCTTTGTTGGACGCGTTCGCGTTTTCGCTTCAATCCCTTGTG	60
QY	61	GTTCATCCCCGACAGAAAGTCCAGTTGTCGAAAGGCTCGGCGTTTCATCGCGCCCTG	120
Db	61	GTTCATCCCCGACAGAAAGTCCAGTTGTCGAAAGGCTCGGCGTTTCATCGCGCCCTG	120
QY	121	ACGCGCGGTTTGAATATTTTATTTCCCTTTATCGACGCGTTCGCTTACCGCATTCGCTG	180
Db	121	ACGCGCGGTTTGAATATTTTATTTCCCTTTATCGACGCGTTCGCTTACCGCATTCGCTG	180
QY	181	AAAGAAATCCCTTTAGACGTACCCGACGAGTCTGCATACGCGCGATTAATACGCAATTG	240
Db	181	AAAGAAATCCCTTTAGACGTACCCGACGAGTCTGCATACGCGCGATTAATACGCAATTG	240
QY	241	ACTGTTGACGCGATCATCTATTTCGAAGTAACCGATCCCAAACTGCGCTCATACGCTTCG	300
Db	241	ACTGTTGACGCGATCATCTATTTCGAAGTAACCGATCCCAAACTGCGCTCATACGCTTCG	300
QY	301	AGCAACTACATTAATGGAATTAACCAAGCTTGCCCAAGACGCGTTCGCTTATCGGG	360
Db	301	AGCAACTACATTAATGGAATTAACCAAGCTTGCCCAAGACGCGTTCGCTTATCGGG	360
QY	361	CGTATGAGTTTGACAAACGTTTGAAGACCGGACGAAATACAGTACGTCGCTTC	420
Db	361	CGTATGAGTTTGACAAACGTTTGAAGACCGGACGAAATACAGTACGTCGCTTC	420
QY	421	GGCCCTGATGAGACGCGCGGCGGCTTGCGGCTGGAAGTCTCGTTACGAATCAAGAT	480
Db	421	GGCCCTGATGAGACGCGCGGCGGCTTGCGGCTGGAAGTCTCGTTACGAATCAAGAT	480
QY	481	TTGTTGTCGCGCCGAAGAAATCCTTTCGCGCAATGACGACCAATTAACGCGCAACGCGA	540
Db	481	TTGTTGTCGCGCCGAAGAAATCCTTTCGCGCAATGACGACCAATTAACGCGCAACGCGA	540
QY	541	AAACGCGCGGATTTATGCGGAATCCGAAGCGCTTAATATGAAACAATCAACTTTCGCAAT	600
Db	541	AAACGCGCGGATTTATGCGGAATCCGAAGCGCTTAATATGAAACAATCAACTTTCGCAAT	600
QY	601	GGTCAGCGTGAAGCGGAATCCGAACATCCGAAGCGAGGCTCAGGCTGCGTCAATGCG	660
Db	601	GGTCAGCGTGAAGCGGAATCCGAACATCCGAAGCGAGGCTCAGGCTGCGTCAATGCG	660
QY	661	TCCAAATGCGGAAGAAATCGCCCGCATCAACGCGCCAAAGGCGAAACGCGAATCCCTGCGC	720
Db	661	TCCAAATGCGGAAGAAATCGCCCGCATCAACGCGCCAAAGGCGAATCCCTGCGC	720
QY	721	CTTTGTTGCCGAAGCCAAATGCGCAAGCATCCGTCAAATTTGCCGCGCTTCAAAACCCA	780
Db	721	CTTTGTTGCCGAAGCCAAATGCGCAAGCATCCGTCAAATTTGCCGCGCTTCAAAACCCA	780
QY	781	GGCGGGGGCGATGCGGTCAATCTGAAGATTTGGGAAACAATATAGTACGCGCTTCAACAT	840
Db	781	GGCGGGGGCGATGCGGTCAATCTGAAGATTTGGGAAACAATATAGTACGCGCTTCAACAT	840
QY	841	CTTGCCAAAGAAAGCAATACGCTGATTTATGCCCCCAATTTGGCCGACATCGGACGCTG	900
Db	841	CTTGCCAAAGAAAGCAATACGCTGATTTATGCCCCCAATTTGGCCGACATCGGACGCTG	900
QY	901	ATTTTCGCGCGATGAAATTTATCGACAGCAAGAAACCGCCAAATTA	948
Db	901	ATTTTCGCGCGATGAAATTTATCGACAGCAAGAAACCGCCAAATTA	948
RESULT 28			
LOCUS	AF226522	948 bp	DNA linear BCT 11-MAR-2000
DEFINITION	Neisseria meningitidis strain Bz169 membrane protein GNA1220		

	(gnaI220) gene, complete cds.
ACCESSION	Af226522
VERSION	Af226522.1 GI:7228872
KEYWORDS	.
SOURCE	Neisseria meningitidis
ORGANISM	Neisseria meningitidis Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.
REFERENCE	1 (bases 1 to 948) Piazza,M., Scarlato,V., Masiagnani,V., Giuliani,M.M., Arico,B., Commanducci,M., Jennings,G.T., Baldi,L., Bartolini,E., Capechi,B., Galeotti,C.L., Luzzi,E., Manetti,R., Marchetti,E., Mora,M., Nuti,S., Ratti,G., Santini,L., Savino,S., Scarselli,M., Storni,E., Zuo,P., Broecker,M., Hundt,K., Knapp,B., Blair,E., Mason,T., Tettelin,H., Hood,D.W., Jeffries,A.C., Saunders,N.J., Granoff,D.M., Venter,C., Moxon,E.R., Grandi,G. and Rapunoli,R. Identification of vaccine candidates against serogroup B <i>Meningococcus</i> by whole-genome sequencing Science 287 (5459), 1816-1820 (2000)
TITLE	
JOURNAL MEDLINE	20175756
PUBMED	10710308
REFERENCES	2 (bases 1 to 948)
AUTHORS	Piazza,M., Masiagnani,V., Commanducci,M., Tettelin,H. and Rapunoli,R.
TITLE	Direct Submission
JOURNAL	Submitted (19-JUN-2000) IRS Immunobiological Research Institute in Stena, Chiron Spa, Via Pioletina, 1, Stena 53100, Italy
FEATURES	Location/Qualifiers
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gene	1..948 /gene="gnaI220"
CDS	1..948 /gene="gnaI220" /note="similar to stomatin-like proteins; Genome-derived <i>Neisseria Antigen GNA1220</i> " /codon_start=1 /transl_table=11 /product="membrane protein GNA1220" /protein_id="AAF42670.1" /db_xref="GI:7228873" /translation="MEFPFILLVAVAFEFKSFVVIPQEVHVVERLGRFRALTAGI NILPLDRVAVRSLKEILPDVPSCVTIDNTQLIVDGLIFQVDLPKLAYSSS YIMATLOAOTLRISVGRELDPFEREDINSTVNVALDEAGAMGVLYRLEIKY LVPROBITRSMOQTTREREGARLABSEBKIRGINLASQRREAIIOOSGEAOANA NASNEKTARKLNRAKGAEASRLVLVEANAEMRIQAALAQTGGADVANLKIAEITYVA APNNLAKESENTLMPENAVADIIGSLISAKMKIIDSKTKAK"
ORIGIN	
Query Match	92.6%; Score 877.6; DB 1; Length 948;
Best Local Similarity	95.4%; Pred. No. 2.3e-197;
Matches 904; Conservative	0; Mismatches 44; Indels 0; Gaps 0.
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Dd	61 GTCATCCACAACAGAAAGTCCAGCGTTGTCCGAAAAAGCTCGGGCGCTTTCATATGCCCCTG 120
Oy	121 ACGCGCGTTTGAATAATTTGATTCCTTATTCGACCAGCGGTCCATACCGCATTCGGCTG 180
Dd	121 ACGCGCGTTTGAATAATTTTGAATTCCTTATTCGACCAGCGGTCCATACCGCATTCGGCTG 180
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Dd	181 AAAGAAATCCCTTTAGACGTACCAGCACGAGTCTGCATACACGCGCATTAATACGAAATYC 240
Oy	241 ACTGTGACGCGCATCATCTAATTTCCAGTAACCATCCCAACTCGCTCATACGTTTC 300

Db	241	ACTGTTGACGGCAATCTATTCTTTTCCAAGTAAACGACCCCAAACTCGCCTCATACAGGTTGC	300
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Db	301	AGCAACTACATTATATGSGAATTACCCAGCTTGCCCAACGACGCTGCTTCCGTATATGGG	360
Qy	361	CGTATGGAAGTTGGACAAAAGTTTGAAGAACGCGACGAATAATCAACAGTACGTCGTC	420
Db	361	CGTATGGAAGTTGGACAAAAGTTTGAAGAACGCGACGAATAATCAACAGTATCTGTTGTCG	420
Qy	421	GCCCTCGATGAGCCGCGCGGCTTTGGGCTGTGTAAGATCTCTCGCTTACGAATCAAGAT	480
Db	421	GCTTTGACACAGCGCGCGCGGCTTTGGGCTGTGTAAGATTTTGCGTTATGAGATTAAAGAC	480
Qy	481	TTGGTTCCGCGCGCAAGAAATCTTTCGCGCAATGCGACCAATTTACCGCCGAACGGAA	540
Db	481	TTGGTTCCGCGCGCAAGAAATCTTTCGCTCAATGCGACCGCAAAATTTACGCGAAGCGAA	540
Qy	541	AAAGCGCCCGCTATATGCGCAATCCGAAGGCGCTAAATTCGAACAAATCAACCTTGCCAGT	600
Db	541	AAAGCGCCCGCTATATGCGCAATCCGAAGGCTGTAAATTCGAACAAATCAACCTTGCCAGT	600
Qy	601	GGTGAGCGTGAGCGCAATTCGAATCCGAAGCGAGCTCGAGCTGCGSTCAATGCG	660
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Qy	661	TCGAATGCGCGAAGAAATGCGCCGATCAACCGCGCCCAAGGCGAAGGGAATCCCTGCGC	720
Db	661	TCAATGCGCGAAGAAATGCGCCGATCAACCGCGCCCAAGGCTGAAGCGGAATCCTTGCGC	720
Qy	721	CTTGTTGCGCGAAGCAATGCGCAAGCCATCCGTCAATTTGCGCGCGCTTCAAAACCAA	780
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Qy	781	GGCGGCGCGATGCGGCTCATCTGAAGATTGCGGAACAATACGTGCGTTCACAGAT	840
Db	781	GGCGGCGCGATGCGGCTCATCTGAAGATTGCGGAACAATACGTGCGTTCACAGAT	840
Qy	841	CTTGCCCAAGAACCAATACGCTGATTATGCGCGCCCAATGTTGCGCATGCGAGCCTG	900
Db	841	CTTGCCCAAGAACCAATACGCTGATTATGCGCGCCCAATGTTGCGCATGCGAGCCTG	900
Qy	901	ATTTCGCGCGCATGAAATTTATGACACGACGCAAAACCGCCAAATTA	948
Db	901	ATTTCGCGCGCATGAAATTTATGACACGACGCAAAACCGCCAAATTA	948
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LOCUS			
DEFINITION	Neisseria meningitidis strain Bz83	membrane protein GNA1220	
ACCESSION	AF226525		
VERSION	AF226525.1	GI:7228878	
KEYWORDS			
SOURCE	Neisseria meningitidis		
ORGANISM	Neisseria meningitidis		
REFERENCE			
AUTHORS	Pizza, M., Scarlato, V., Maignani, V., Giuliani, M.M., Arico, B., Comanducci, M., Jemmings, G.T., Baldi, L., Battolini, E., Capechi, B., Galeotti, C.L., Luzzi, E., Manetti, R., Marchetti, E., Mora, M., Nuti, S., Ratti, G., Santini, L., Savino, S., Scarselli, M., Storni, E., Zuo, P., Broecker, M., Hundt, E., Knapp, B., Blair, E., Mason, T., Tettelin, H., Hood, D.W., Jeffries, A.C., Saunders, N.J., Granoff, D.M., Venter, C., Moxon, E.R., Grandi, G. and Kappun, R.		
TITLE	Identification of vaccine candidates against serogroup B meningococcus by whole-genome sequencing		
JOURNAL	Science 287 (5459), 1816-1820		
MEDLINE	2017576		
PUBMED	10710308		

REFERENCE 2 (bases 1 to 948)
 AUTHORS Pizze M., Masignani V., Comanducci M., Tettelin H. and Rappunli R.
 TITLE Direct Submission
 JOURNAL Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in
 Siena, Chiron Spa, Via Fiorentina, 1, Siena 53100, Italy
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ORIGIN

Query Match 92.6%; Score 877.6; DB 1; Length 948;
 Best Local Similarity 95.4%; Pred. No. 2,3e-197;
 Matches 904; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 1 ATGGAATTTTCTATTCTTTGTTGGAGCGGTCGCGTTTGGCTTCAATCTTTGTC 60
 DB 1 ATGGAATTTTCTATTCTTTGTTGGAGCGGTCGCGTTTGGCTTCAATCTTTGTC 60

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QY 901 ATTTCTGCGCGATGAATTAATTCGACGACGACCAAAACCGCAATPA 948
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RESULT 30
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 LOCUS Neisseria meningitidis strain H44/76 membrane protein GNA1220
 DEFINITION (gna1220) gene, complete cds.
 ACCESSION AF226529
 VERSION AF226529.1 GI:7228886
 KEYWORDS
 ORGANISM
 Neisseria meningitidis
 Neisseria meningitidis
 Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 Neisseriaceae; Neisseria.

REFERENCE
 AUTHORS Pizze M., Scarlato V., Masignani V., Giuliani M.M., Arico B.,
 Comanducci M., Deming G.T., Balle L., Barcolini E., Capocchi B.,
 Galeotti C.L., Luzzi B., Manetti R., Marchetti B., Mora M.,
 Nuti S., Ratti G., Santini L., Savino S., Scarselli M., Stormi E.,
 Zuo P., Brocker M., Hundt E., Knapp B., Blair E., Mason T.,
 Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M.,
 Venter C., Moxon E.R., Grandi G. and Rappunli R.
 Identification of vaccine candidates against serogroup B
 meningococcus by whole-genome sequencing
 Science 287 (5459), 1816-1820 (2000)

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 20175756
 10710308

REFERENCE
 2 (bases 1 to 948)
 AUTHORS Pizze M., Masignani V., Comanducci M., Tettelin H. and Rappunli R.
 TITLE Direct Submission
 JOURNAL Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in
 Siena, Chiron Spa, Via Fiorentina, 1, Siena 53100, Italy
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ORIGIN

Query Match 92.6%; Score 877.6; DB 1; Length 948;
 Best Local Similarity 95.4%; Pred. No. 2.3e-197;
 Matches 904; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 1 ATGGAATTTTCTATCTTTGTTGACGCGCGCTTTCGGCTTCAATCCTTTGTC 60
 DB 1 ATGGAATTTTCTATCTTTGTTGTTGACGCGCGCTTTCGGCTTCAATCCTTTGTT 60

QY 61 GTCAATCCCCAGAGAGATCCACGTTGCGAAAGCTGGGGGCTTCCATCGCGCCCTG 120
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RESULT 31

AP226530

948 bp DNA linear BCT 11-MAR-2000

LOCUS AP226530 948 bp DNA linear BCT 11-MAR-2000
 DEFINITION Neisseria meningitidis strain MC58 membrane protein GNA1220
 (gna1220) gene, complete cds.

ACCESSION AP226530
 VERSION AP226530.1 GI:7228888

KEYWORDS
 SOURCE

ORGANISM
 Neisseria meningitidis
 Neisseria meningitidis
 Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 Neisseriaceae; Neisseria.

REFERENCE

1 (bases 1 to 948)
 Pizza, M., Scarlato, V., Masignani, V., Giuliani, M.M., Arico, B.,
 Comanducci, M., Jennings, G.T., Baldi, L., Barcolini, E., Capocchi, B.,
 Galeotti, C.L., Luzzi, E., Manetti, R., Marchetti, B., Mora, M.,
 Nuti, S., Ratti, G., Santini, L., Savino, S., Scarselli, M., Stormi, E.,
 Zuo, P., Broeker, M., Hundt, E., Knapp, B., Blair, E., Mason, T.,
 Tettelin, H., Hood, D.W., Jeffries, A.C., Saunders, N.J., Granoff, D.M.,
 Venter, C., Woxon, E.R., Grandi, G. and Rappelli, R.

TITLE
 Identification of vaccine candidates against serogroup B
 meningococcus by whole-genome sequencing
 JOURNAL
 Science 287 (5459), 1816-1820 (2000)

MEDLINE
 PUBMED
 10710308

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in
 Siena, Chiron SpA, Via Fiorentina, 1, Siena 53100, Italy

FEATURES

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CDS

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Db	781	GGCGGGGGCGGATGCGGTCATCTGAAGATTGGGGAACATAGTAGCCCGCTTCAACAT	840
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Qy	901	ATTTCGCGCGCATGAAATTTATCGACAGACGCAAAACCGCCAAATTA	948
Db	901	ATTTCGCGCGCATGAAATTTATCGACAGACGCAAAACCGCCAAATTA	948
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DEFINITION	Neisseria meningitidis strain SW2107 membrane protein GNA1220 (gna1220)	gene, complete cds.	
ACCESSION	AF226540		
VERSION	AF226540.1	GI:7228908	
KEYWORDS	Neisseria meningitidis		
SOURCE	Neisseria meningitidis		
ORGANISM	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.		
REFERENCE			
AUTHORS	1 (bases 1 to 948)		
	Pizza, M., Scarlato, V., Masignani, V., Giuliani, M.M., Arico, B., Comanducci, M., Jennings, G.T., Baldi, L., Bartolini, E., Capecci, B., Galeotti, C.L., Iuzzi, E., Manetti, R., Marchetti, E., Mora, M., Nuti, S., Ratti, G., Santini, L., Savino, S., Scarselli, M., Storni, E., Zuo, P., Broeker, M., Hunte, E., Knapp, B., Blair, E., Mason, T., Tettelin, H., Hood, D.W., Jeffries, A.C., Saunders, N.D., Granoff, D.M., Venter, C., Moxon, E.R., Grandi, G., and Rappuoli, R.		
	Identification of vaccine candidates against serogroup B meningococcus by whole-genome sequencing		
	Science 287 (5459), 1816-1820 (2000)		
JOURNAL	20175756		
MEDLINE	10710308		
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AUTHORS	Pizza, M., Masignani, V., Comanducci, M., Tettelin, H. and Rappuoli, R.		
TITLE	Direct Submision		
JOURNAL	Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in Siena, Chiron Spa, Via Fiorentina, 1, Siena 53100, Italy		
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		Best Local Similarity 95.4%; Pred. No. 2.3e-197;	
		Matches 904; Conservative 0; Mismatches 44; Indels 0; Gaps 0;	
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Qy	121	ACGCGCGGTTTGAATTTTGAATTCCTTTATCGAACCGGTGTCTTACCGCATTCGCTG	180
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Qy	901	ATTTCGCGCGCATGAAATTTATCGACAGACGCAAAACCGCCAAATTA	948
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DEFINITION	Sequence 14 from Patent WO0066791.		
ACCESSION	AX043935		

VERSION AX043935.1 GI:11342857
 KEYWORDS
 SOURCE Neisseria meningitidis
 ORGANISM Neisseria meningitidis
 Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 Neisseriaceae; Neisseria.
 REFERENCE
 AUTHORS 1 Pizzo, M., Hickey, E., Peterson, J., Tettelin, H., Venter, J. C.,
 Masiugnani, V., Galeotti, C., Mora, M., Ratti, G., Scarlati, M.,
 Scarlato, V., Rappunli, R., Frazer, C. M., and Grandi, G.
 Neisseria genomic sequences and methods of their use
 Patent: WO 0065791-A 14 09-NOV-2000;
 CHIRON CORPORATION (US) THE INSTITUTE FOR GENOMIC RESEARCH (US)
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 Best Local Similarity 95.4%; Pred. No. 2.3e-197;
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 VERSION AE002470.1 GI:7226457
 KEYWORDS
 SOURCE
 ORGANISM
 Neisseria meningitidis MCS8
 Neisseria meningitidis MCS8
 Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 Neisseriaceae; Neisseria.
 REFERENCE
 AUTHORS 1 (bases 1 to 10144)
 Tettelin, H., Saunders, N. J., Heidelberg, J., Jeffries, A. C.,
 Nelson, K. E., Eisen, J. A., Ketchum, K. A., Hood, D. W., Peden, J. P.,
 Dodson, R. J., Nelson, W. C., Gwinn, M. L., Deboy, R., Peterson, J. D.,
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 Pizzo, M., Grandi, G., Sun, L., Smith, H. O., Frazer, C. M., Moxon, E. R.,
 Rappunli, R., and Venter, J. C.
 Complete genome sequence of Neisseria meningitidis serogroup B
 strain MCS8
 JOURNAL Science 287 (5459), 1809-1815 (2000)
 MEDLINE 20175755
 PUBMED 10710307
 REFERENCE
 AUTHORS 2 (bases 1 to 10144)
 Tettelin, H., Saunders, N. J., Heidelberg, J., Jeffries, A. C.,
 Nelson, K. E., Eisen, J. A., Ketchum, K. A., Hood, D. W., Peden, J. P.,
 Dodson, R. J., Nelson, W. C., Gwinn, M. L., Deboy, R., Peterson, J. D.,
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 Rappunli, R., and Venter, J. C.
 Direct Submission
 Submitted (17-MAR-2000) The Institute for Genomic Research, 9712
 Medical Center Dr, Rockville, MD 20850, USA
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 JOURNAL
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 Neisseria meningitidis
 Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
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 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 FEATURES
 Location/Qualifiers

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ACCESSION AX044032.1 GI:11342916
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ORGANISM
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Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
REFERENCE
AUTHORS
1 Pizza, M., Hickey, E., Peterson, J., Tettelin, H., Venter, J.C.,
Masignani, V., Galeotti, C., Mora, M., Ratti, G., Scarlato, V.,
Scarlato, V., Rappuoli, R., Frazer, C.M. and Grandi, G.,
Neisseria genomic sequences and methods of their use
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CHIRON CORPORATION (US); THE INSTITUTE FOR GENOMIC RESEARCH (US)
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ORIGIN
Query Match 92.6%; Score 877.6; DB 6; Length 349980;
Best local similarity 95.4%; Pred. No. 2.7e-197;
Matches 904; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
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ACCESSION
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VERSION
AF226526.1 GI:7228880
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Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
REFERENCE
AUTHORS
1 Pizza, M., Scarlato, V., Masignani, V., Giuliani, M.M., Arico, B.,
Comanducci, M., Jennings, G.T., Baldi, L., Bartoloni, B., Capechi, B.,
Galeotti, C.L., Luzzi, E., Manetti, R., Marchetti, B., Mora, M.,
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Zuo, P., Brooker, M., Hundt, E., Knapp, B., Blair, E., Mason, T.,
Tettelin, H., Hood, D.W., Jeffries, A.C., Saunders, N.J., Granoff, D.M.,
Venter, C., Moxon, E.R., Grandi, G. and Rappuoli, R.
Identification of vaccine candidates against serogroup B
meningococcus by whole-genome sequencing
Science 287 (5459), 1816-1820 (2000)
JOURNAL
MEDLINE
10710308
PUBMED
20175756
REFERENCE
2 (bases 1 to 948)
AUTHORS
Pizza, M., Masignani, V., Comanducci, M., Tettelin, H. and Rappuoli, R.
TITLE
Direct Submission
JOURNAL
Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in
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Best Local Similarity 95.3%; Pred. No. 5.4e-197;
Matches 903; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

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RESULT 40
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ACCESSION
AF226535
VERSION
AF226535.1 GI:7228898
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Neisseria meningitidis
Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
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1 (bases 1 to 948)
Pizza, M., Scarlato, V., Masignani, V., Giuliani, M.M., Arico, B.,
Comanducci, M., Jennings, G.T., Baldi, L., Bartoloni, E., Capecechi, B.,
Galeotti, C.L., Iuzzo, E., Manetti, R., Marchetti, B., Mora, M.,
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2 (bases 1 to 948)
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Direct Submission
Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in
Stena, Chiron Spa, Via Fiorentina, 1, Stena 53100, Italy
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